

# SEARCH REQUEST FORM

Scientific and Technical Information Center

Requestor's Name: David Lukton    Examiner number: 71263    Date: 5/24/04

Art Unit: 1653    Phone number: 571-272-0952    Serial Number:  
09-765105

Mail Box: 3-C-70    Examiner Rm: 3-B-75    Results format: paper

\* \* \* \* \*

Title of Invention: C-TERMINAL MODIFIED OXAMYL  
DIPEPTIDES AS INHIBITORS OF THE ICE-CED-3 FAMILY OF  
CYSTEINE PROTEASES

Applicants: KARANEWSKY, DONALD S., TERNANSKY, ROBERT  
J., LINTON, STEVEN D., DINH, THANG

Earliest Priority Date: 7/2/98

\* \* \* \*

Please search the sequences in this case

182 1A3

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher:		NA Sequence (#)	STN
Searcher Phone #:		AA Sequence (#)	Dialog
Searcher Location:		Structure (#)	Questel/Orbit
Date Searcher Picked Up	5/24/04	Bibliographic	Dr. Link
Date Computed:	5/25/04	Litigation	Lexis/Nexis
Searcher Prep & Review Time		Fulltext	Sequence Systems
Clerical Prep Time		Patent Family	QSP
Online Use		Other	WWW/Internet

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

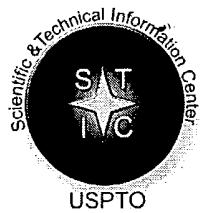
Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions

**.rnpm and .rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions

**.rapm and .rapn**

***Because they contain data that is confidential, the results of Pending database searches should not be left in the case .***



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 122770

**TO:** David Lukton  
**Location:** rem/3b75/3c70  
**Art Unit:** 1653  
**Tuesday, May 25, 2004**

**Case Serial Number:** 09/765105

**From:** Edward Hart  
**Location:** Biotech-Chem Library  
**REM-1A55**  
**Phone:** 571-272-2512

**edward.hart@uspto.gov**

### Search Notes

Examiner Lukton,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



# STIC SEARCH RESULT FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor  
571-272-2507 Remsen E01 D86

### Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:*  Example: 1610

➤ *Relevant prior art found, search results used as follows:*

- 102 rejection
- 103 rejection
- Cited as being of interest.
- Helped examiner better understand the invention.
- Helped examiner better understand the state of the art in their technology.

*Types of relevant prior art found:*

- Foreign Patent(s)
- Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- Results verified the lack of relevant prior art (helped determine patentability).
- Results were not useful in determining patentability or understanding the invention

**Comments:**

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



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OM Protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 51 Seconds  
(without alignments)

22.161 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: Geneseq\_29Jan04:\*
- 2: GeneseqP\_1908:\*
- 3: GeneseqP\_2000B:\*
- 4: GeneseqP\_2001:\*
- 5: GeneseqP\_2002:\*
- 6: GeneseqP\_2003as:\*
- 7: GeneseqP\_2003bs:\*
- 8: GeneseqP\_2004s:\*

26 21 100.0 4 3 AAY99959 Tetrapapt  
27 21 100.0 4 3 AAY49941 Synthetic  
28 21 100.0 4 3 AAB26850 Synthetic  
29 21 100.0 4 3 AAY80783 Fluoropho  
30 21 100.0 4 3 AAY69867 ICE cleav  
31 21 100.0 4 3 AAY67492 Caspase 1  
32 21 100.0 4 3 AAY81938 APP agoni  
33 21 100.0 4 3 AAY87640 Caspase 1  
34 21 100.0 4 3 AAB26703 Caspase S  
35 21 100.0 4 3 AAB03094 Substrate  
36 21 100.0 4 3 AAY56899 Caspase i  
37 21 100.0 4 3 AAY57442 Peptide A  
38 21 100.0 4 3 AAB28539 Caspase-1  
39 21 100.0 4 3 AAB32119 Tetrapapt  
40 21 100.0 4 4 AAB59584 Caspase-1  
41 21 100.0 4 4 AAG62548 Cresyl vi  
42 21 100.0 4 4 AAG67379 Peptide S  
43 21 100.0 4 4 AAY72472 YVAD Pept  
44 21 100.0 4 4 AAG64408 Caspase P  
45 21 100.0 4 4 AAB91890 Apoptosis

#### ALIGNMENTS

RESULT 1  
AAR34789  
ID AAR34789 standard; peptide; 4 AA.

XX  
AC AAR34789;  
XX  
XX DT 25-MAR-2003 (revised)  
XX DT 08-JUL-1993 (first entry)  
DE Interleukin-1beta convertase activity determining peptide.  
XX ICE; interleukin-1beta convertase; activity; chromophore contg;  
XX monitoring; IL-1 mediated diseases; ICE inhibitor evaluation; diagnosis.  
XX  
OS Synthetic.  
XX  
PH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-acetyl-Tyr"  
FT Modified-site 4  
FT /note= "Asp-P-nitroanilide, Asp-6-aminoquinoline amide"  
FT /note= "Asp-7-amino-4-methylcoumarin amide"  
XX  
XX EP532226 A2.  
XX  
PD 24-MAR-1993.  
XX  
PF 08-AUG-1992; 92EP-00202449.  
XX  
PR 16-AUG-1991; 91US-00746554.  
XX  
PR 17-DEC-1991; 91US-00808996.  
XX  
(MERCK & CO INC.  
XX  
PI Chapman KT, Macoss M, Mumford RA, Thornberry NA, Weidner JR;  
XX  
DR WPI: 1993-095331/12.  
XX  
PT New chromophore-contg. Peptide derivs. - for determining interleukin-1-  
beta convertase activity in the diagnosis of inflammatory and immune-  
based conditions.  
XX  
PS Example; Page 26; 41pp; English.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	21	AAR34789	4	2	AAR34621	Aar34789 Interleuk
2	21	100.0	4	2	AAR32544	Aar34621 Chromopio
3	21	100.0	4	2	AAR34622	Aar34622 Chromopio
4	21	100.0	4	2	AAR51047	Aar51047 Sequence
5	21	100.0	4	2	AAR77200	Aar77200 Cell pro1
6	21	100.0	4	2	AAR5702	Aar5702 Tetrapapt
7	21	100.0	4	2	AAR98753	Aar8753 Asp-ase 1
8	21	100.0	4	2	Aaw00214	Aaw00214 Ich-2 sub
9	21	100.0	4	2	Aaw06453	Aaw06453 ICE pept1
10	21	100.0	4	2	Aaw5979	Aaw5979 Cysteine
11	21	100.0	4	2	Aaw76199	Aaw76199 Mouse cas
12	21	100.0	4	2	Aaw52749	Aaminomech
13	21	100.0	4	2	Abp1236	Abp1236 ICE-speci
14	21	100.0	4	2	Aaw65304	Aaw65304 Peptide C
15	21	100.0	4	2	Aaw565067	Aaw565067 ICE bindi
16	21	100.0	4	2	Aay15619	Aay15619 Peptide u
17	21	100.0	4	2	Aay30071	Aay30071 N-substit
18	21	100.0	4	2	Aay04112	Aay04112 Enzyme co
19	21	100.0	4	2	Aaw68555	Aaw68555 Interleuk
20	21	100.0	4	2	Aay24410	Aay24410 Caspase P
21	21	100.0	4	2	Aaw99674	Aaw99674 ICE prote
22	21	100.0	4	2	Aaw24092	Aaw24092 Protease
23	21	100.0	4	2	Aaw94094	Aaw94094 Protease
24	21	100.0	4	3	Aay9647	Aay9647 Caspase 1
25	21	100.0	4	3		

The peptide is a chromophore-contg. compound which is useful in determining interleukin-1 (ICE) activity and is therefore useful in diagnosis and monitoring of IL-1 mediated diseases or in evaluation of ICE inhibitors. IL-1 has been implicated in meningitis, encephalitis and septic shock.

CC salpingitis, complications of septic shock, disseminated intravascular coagulation; adult respiratory distress syndrome, inflammation due to antigen, antibody, and/or complement deposition, arthritis, cholangitis, CC colitis, encephalitis, endocarditis, glomerulonephritis, hepatitis, CC myocarditis, pericarditis, pancreatitis, perfusion injury, and vasculitis. Immune based diseases include hypersensitivity, graft rejection, graft-v-host disease, and autoimmune diseases including Type I diabetes mellitus and multiple sclerosis. IL-1 has also been implicated in treatment of bone and cartilage resorption, or diseases causing excessive extracellular matrix deposition. These include periodontal disease, interstitial pulmonary fibrosis, cirrhosis, systemic sclerosis, or keloid formation. To use the peptide in an assay, the peptide, ICE, the biological sample, and an aminopeptidase (APase) are mixed. The APase cleaves the chromophore bond, and the ICE activity is then determined by spectrophotometric or fluorimetric analysis. Leucine amino-peptidase (LAPM) is the most preferred enzyme in the disclosure. The peptide is used in concns. of 1  $\mu$ M to 10 mM. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYAD 4  
Db 1 YYAD 4

RESULT 2  
AAR34621 ID AAR34621 standard; peptide; 4 AA.  
XX AC AAR34621;  
XX DT 25-MAR-2003 (revised)  
XX DT 12-NOV-1992 (first entry)

DE Chromophore-contg. cpd. for determining ICE activity (1).  
XX Interleukin-1beta; IL-1b; inflammation; immune; disease; diagnosis;  
KW p-nitroanilide.  
XX Synthetic.

XX Key Location/Qualifiers  
PT Modified-site 1 /note= "N-acetyl-tyrosinyl"  
PT Modified-site 4 /note= "aspartic acid 7-amino-4-methylcoumarin"  
XX EP528487-A2.  
XX PD 24-FEB-1993.  
XX DR 08-AUG-1992; 92EP-00202450.  
XX PR 16-AUG-1991; 91US-00746455.  
XX PR 17-DEC-1991; 91US-00808994.  
XX PA (MERI ) MERCK & CO INC.  
XX PI Chapman KT, Thornberry NA, Maccoss M, Weidner JR, Mumford RA;  
PI Hagmann WK;  
XX DR 1993-060350/08.

XX New chromophore-contg. cpds. - for determining interleukin-1beta convertase activity in diagnosis of inflammatory or immune-based disorders.  
XX PS Example 8; Page 31; 42pp; English.

XX PI Chapman KT, Thornberry NA, Maccoss M, Weidner JR, Mumford RA;  
PI Hagmann WK;  
XX DR 1993-060350/08.  
XX New chromophore-contg. cpds. - for determining interleukin-1beta convertase activity in diagnosis of inflammatory or immune-based disorders.  
XX PS Claim 9; Page 42; 42pp; English.

XX The cpd. is used for determining interleukin-1beta convertase (ICE) activity. ICE has been implicated in inflammatory and immune-based diseases including diseases of the lungs and airways, CNS, eyes, ears, joints, bones and connective tissues, cardiovascular system (including the pericardium), GI and urogenital systems and skin and mucosal membranes. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YYAD 4  
Db 1 YYAD 4

RESULT 3  
AAR3544 ID AAR3544 standard; peptide; 4 AA.  
XX AC AAR3544;  
XX DT 25-MAR-2003 (revised)  
XX DT 12-NOV-1992 (first entry)

DE Chromophore-contg. cpd. for determining ICE activity (5).  
XX Interleukin-1beta; IL-1b; inflammation; immune; disease; diagnosis;  
KW 7-amino-4-methylcoumarin.  
XX Synthetic.

XX Key Location/Qualifiers  
PT Modified-site 1 /note= "N-acetyl-tyrosinyl"  
PT Modified-site 4 /note= "aspartic acid 7-amino-4-methylcoumarin"  
XX EP528487-A2.  
XX PD 24-FEB-1993.  
XX DR 08-AUG-1992; 92EP-00202450.  
XX PR 16-AUG-1991; 91US-00746455.  
XX PR 17-DEC-1991; 91US-00808994.  
XX PA (MERI ) MERCK & CO INC.  
XX PI Chapman KT, Thornberry NA, Maccoss M, Weidner JR, Mumford RA;  
PI Hagmann WK;  
XX DR 1993-060350/08.

XX New chromophore-contg. cpds. - for determining interleukin-1beta convertase activity in diagnosis of inflammatory or immune-based disorders.  
XX PS Example 8; Page 31; 42pp; English.

XX The cpd. is used for determining interleukin-1beta convertase (ICE) activity. ICE has been implicated in inflammatory and immune-based diseases including diseases of the lungs and airways, CNS, eyes, ears, joints, bones and connective tissues, cardiovascular system (including the pericardium), GI and urogenital systems and skin and mucosal membranes. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 4 AA;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; OS

Qy 1 YVAD 4  
Db 1 YVAD 4

RESULT 4  
AAR34622 standard; peptide; 4 AA.

ID AAR34622  
AC AAR34622;  
XX DE Chromophore-contg. cpd. for determining ICE activity (2).  
XX OS Synthetic.

XX Key Location/Qualifiers  
FT Modified-site 1 /label= AC  
FT Modified-site 4 /label= CHO

XX WO9406906-A1.  
XX PD 31-MAR-1994.  
XX PP 09-SEP-1993; 93WO-US008479.  
XX PR 18-SEP-1992; 92US-00947330.  
XX PA (MERCK & CO INC.  
XX PI Molineaux SM, Rolando AM, Casano FJ;  
XX DR WPI: 1994-118456/14.  
XX XX DNA encoding murine precursor interleukin 1 beta converting enzyme - For  
PT producing ICE and its subunits and for identification of inhibitors of  
ICE activity.  
XX PS Disclosure; Page 15; 87pp; English.  
XX XX cDNA encoding murine pre-IL-1 beta converting enzyme (ICE) was isolated  
CC from IL-1 producing mouse cells. Murine ICE cleaves the peptide bond  
CC between Asp17 and Val18 of murine precursor IL-1 beta, and the peptide  
CC bond between Asp27 and Gly28. The preferred cells for isolating murine  
CC ICE-encoding DNA include mouse macrophages and (pref.) WEHI-3 cells.  
CC Tetrapeptide aldehyde inhibitor Ac-YVAD-CHO inhibits murine ICE with a Ki  
CC of 3nM or less. This is comparable to the potency observed against the  
CC human enzyme and suggests that the active sites of both convertases are  
CC similar. Ac-YVAD-CHO was used to make an affinity ligand (Ac-YVAD-CHO)  
CC with which to purify active ICE. Due to the enzyme's unusual substrate  
CC specificity, an affinity column can be used to purify ICE in a single  
CC step from a crude cellular lysate. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX SQ Sequence 4 AA;

CC The cpd. is used for determining interleukin-1beta convertase (ICE)  
CC activity. ICE has been implicated in inflammatory and immune-based  
CC diseases including diseases of the lungs and airways, CNS, eyes, ears,  
CC joints, bones and connective tissues, cardiovascular system (including  
CC the pericardium, GI and urogenital systems and skin and mucosal  
CC membranes. (Updated on 25-MAR-2003 to correct PN field.)  
XX SQ Sequence 4 AA;

CC Query Match 100.0%; Score 21; DB 2; Length 4;  
CC Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 1 YVAD 4

RESULT 5  
AAR51047 standard; protein; 4 AA.

ID AAR51047  
DE Cell proliferation enzyme proteinase activity substrate peptide #5.

XX AC AAR51047;  
XX DT 25-MAR-2003 (revised)  
XX DT 07-OCT-1994 (First entry)  
XX DE Sequence of tetrapeptide aldehyde inhibitor of murine precursor  
DE interleukin-1 beta (pre-IL-1 beta) converting enzyme (ICE).  
XX KW Interleukin-1 beta converting enzyme; mature interleukin; inhibitor;  
OS Synthetic.  
XX Key Location/Qualifiers  
FT Modified-site 1 /label= AC  
FT Modified-site 4 /label= CHO

XX WO9406906-A1.  
XX PD 31-MAR-1994.  
XX PP 09-SEP-1993; 93WO-US008479.  
XX PR 18-SEP-1992; 92US-00947330.  
XX PA (MERCK & CO INC.  
XX PI Molineaux SM, Rolando AM, Casano FJ;  
XX DR WPI: 1994-118456/14.  
XX XX DNA encoding murine precursor interleukin 1 beta converting enzyme - For  
PT producing ICE and its subunits and for identification of inhibitors of  
ICE activity.  
XX PS Disclosure; Page 15; 87pp; English.  
XX XX cDNA encoding murine pre-IL-1 beta converting enzyme (ICE) was isolated  
CC from IL-1 producing mouse cells. Murine ICE cleaves the peptide bond  
CC between Asp17 and Val18 of murine precursor IL-1 beta, and the peptide  
CC bond between Asp27 and Gly28. The preferred cells for isolating murine  
CC ICE-encoding DNA include mouse macrophages and (pref.) WEHI-3 cells.  
CC Tetrapeptide aldehyde inhibitor Ac-YVAD-CHO inhibits murine ICE with a Ki  
CC of 3nM or less. This is comparable to the potency observed against the  
CC human enzyme and suggests that the active sites of both convertases are  
CC similar. Ac-YVAD-CHO was used to make an affinity ligand (Ac-YVAD-CHO)  
CC with which to purify active ICE. Due to the enzyme's unusual substrate  
CC specificity, an affinity column can be used to purify ICE in a single  
CC step from a crude cellular lysate. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX SQ Sequence 4 AA;

CC The cpd. is used for determining interleukin-1beta convertase (ICE)  
CC activity. ICE has been implicated in inflammatory and immune-based  
CC diseases including diseases of the lungs and airways, CNS, eyes, ears,  
CC joints, bones and connective tissues, cardiovascular system (including  
CC the pericardium, GI and urogenital systems and skin and mucosal  
CC membranes. (Updated on 25-MAR-2003 to correct PN field.)  
XX SQ Sequence 4 AA;

CC Query Match 100.0%; Score 21; DB 2; Length 4;  
CC Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 1 YVAD 4

RESULT 6  
AAR77200 standard; peptide; 4 AA.  
ID AAR77200  
XX AC AAR77200;  
XX DT 27-FEB-1996 (First entry)  
DE Cell proliferation enzyme proteinase activity substrate peptide #5.

XX Proteinase; cell growth-stimulating protein; hydrolysis;  
 KW macrophage chemotactic action; serine protease inhibitor; wound;  
 KW gastric ulcer; leg ulcer; bed sore.  
 OS Synthetic.

XX Key  
 PT Modified-site 1 Location/Qualifiers  
 FT /label= Acyl-Tyr  
 FT Modified-site 4 /note= "Modified by 4-methyl-coumaryl-7-amide".  
 FT  
 XX EP661293-A2.  
 XX 05-JUL-1995.  
 XX 94EP-00120406.  
 PR 22-DEC-1994; 93JP-00351225.  
 XX (SAW ) SANTWA KAGAKU KENKYUSHO CO.  
 XX PI Yamaguchi T, Uesaka H, Watanabe K, Awaya J;  
 XX WPI; 1995-233274/31.  
 XX Protein derived from Clostridium perfringens FERM BP-4584 - stimulates  
 PT cell proliferation and has macrophage chemotactic action.  
 XX Example: Page 8; 14pp; English.  
 XX The sequences given in AAR7196-200 are peptides which were used to  
 CC demonstrate the proteinase activity of the cell growth-stimulating  
 protein of the invention. The protein was seen to selectively hydrolyse  
 CC synthetic substrates having an aromatic amino acid at the C-terminal. The cell  
 CC response to the peptide given in AAR7196 was particularly high. The cell  
 CC growth-stimulating protein has a mol. wt. of 420 +/- 40 kD and a single  
 CC subunit mol. wt. of 110 +/- 20 kD. It has an isoelectric point of 4.8  
 CC and has cell growth stimulating action and macrophage chemotactic  
 CC action, as well as proteinase activity. Its enzymatic activity decreases  
 CC in the presence of a serine protease inhibitor, increase in the presence  
 CC of various metal ions, and is stabilised in the presence of calcium ion.  
 CC The protein is particularly useful for the treatment of wounds, gastric  
 CC and leg ulcers, eg. bed sores

XX Sequence 4 AA;  
 XX Query Match 100.0%; Score 21; DB 2; Length 4;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 Qy 1 YVAD 4  
 DB 1 YVAD 4  
 XX Sequence 4 AA;  
 XX Query Match 100.0%; Score 21; DB 2; Length 4;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
 DB 1 YVAD 4  
 XX Sequence 4 AA;  
 XX Query Match 100.0%; Score 21; DB 2; Length 4;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 Qy 1 YVAD 4  
 DB 1 YVAD 4  
 XX Sequence 4 AA;  
 XX Query Match 100.0%; Score 21; DB 2; Length 4;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
 DB 1 YVAD 4  
 XX Sequence 4 AA;  
 XX Query Match 100.0%; Score 21; DB 2; Length 4;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Modified-site 1 /note= "N-terminal acetyl gp."  
 PT  
 XX WO9535367-A1.  
 PN  
 XX 28-DEC-1995.  
 PD  
 XX 16-JUN-1995; 95WO-US007619.  
 PT  
 XX 17-JUN-1994; 94US-00261582.  
 FT  
 XX (VERT-) VERTEX PHARM INC.  
 PA  
 XX Wilson KP, Griffith JP, Kim EE, Livingston DJ;  
 PI  
 XX DR; WPI; 1995-058405/06.  
 XX Interleukin-1 beta converting enzyme (ICE) crystal structure - useful for  
 PT design and evaluating cpts., esp. inhibitors that bind to ICE active  
 PT site or accessory binding site.  
 XX Example 1; Page 33; 104pp; English.  
 XX A tetrapeptide aldehyde (AAR95702) used in 2x molar excess completely  
 CC inhibited the activity of autoprocessed interleukin-1 beta converting  
 enzyme (ICE) (see also AAR95701, obt. by expression of human ICE cDNA in  
 CC Escherichia coli). The protein-inhibitor complex was purified, and  
 CC crystals of ICE in complex with the inhibitor were grown by vapour  
 CC diffusion. These were used to determine the crystal structure of ICE.  
 CC useful e.g. in the design of novel ICE inhibitors  
 XX Sequence 4 AA;  
 XX Query Match 100.0%; Score 21; DB 2; Length 4;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 Qy 1 YVAD 4  
 DB 1 YVAD 4  
 XX Sequence 4 AA;  
 XX Query Match 100.0%; Score 21; DB 2; Length 4;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 Qy 1 YVAD 4  
 DB 1 YVAD 4  
 XX Sequence 4 AA;  
 XX Query Match 100.0%; Score 21; DB 2; Length 4;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 Qy 1 YVAD 4  
 DB 1 YVAD 4  
 XX Sequence 4 AA;  
 XX Query Match 100.0%; Score 21; DB 2; Length 4;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PI Horvitz HR, Yuan J, Shaham S;  
 XX WPI: 1996-425082/42.  
 DR Ced-3 and human interleukin 1-beta convertase genes and proteins - useful  
 PT to treat inflammation and diseases characterised by cell death.  
 XX Claim 7; Page 94; 139pp; English.

CC A peptide aldehyde including the sequence given in AAR98752, and a  
 CC peptide aldehyde designated 'inhibitor B' (AAR98753), are effective,  
 CC specific and reversible inhibitors of the protease activity of human  
 CC interleukin-1 beta converting enzyme (ICE) (AAR98755) and related  
 CC proteases such as nematode Ced-3 (AAR98754). They are thought to act as  
 CC transition analogues, which compete for ICE binding to its substrate, pro  
 CC -interleukin-1 beta; the Ki for inhibitor B is 0.76 nM. The peptide  
 CC aldehydes (Aspase inhibitors) inhibit the death of human nerve cells  
 CC including motoneurons, and can be used to prevent/decrease cell deaths  
 CC due to amyotrophic lateral sclerosis, spinal cord injury, Parkinsonism  
 CC Huntington's disease, Alzheimer's disease or spinocerebellar degeneration  
 XX

SQ Sequence 4 AA;  
 Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YYAD 4  
 Db 1 YYAD 4

RESULT 10  
 AAW0453 standard; peptide; 4 AA.  
 ID AAW0453  
 XX  
 AC AAW0453;  
 XX  
 DT 03-MAR-1997 (first entry)  
 DE ICE peptide substrate.  
 XX  
 KW Ced-3/Ice; cysteine protease; apoptosis; autoimmune disease;  
 KW cancer; HIV; Alzheimer's disease; therapy.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9636698-A1.  
 XX  
 PD 21-NOV-1996.  
 XX  
 PP 16-MAY-1996;  
 XX  
 PR 03-MAR-1997.  
 XX  
 DR ICE peptide substrate.  
 XX  
 PA 96WO-US007010.  
 XX  
 PR 18-MAY-1995;  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 PR New isolated apoptotic cysteine protease, Mch 2 - used to develop prods.  
 XX  
 PR for use as anti-apoptotic agents or as cytotoxic agents.  
 XX  
 PI Litwack G, Alnemri ES, Fernandez-Alnemri T;  
 XX  
 DR WPI; 1997-012077/01.  
 XX  
 PR Disclosure; Page 28; 43pp; English.  
 XX  
 A tetrapeptide (AAW0453) is the interleukin-1 beta converting enzyme  
 CC (ICE) cleavage site in pro-interleukin-1 beta. Another tetrapeptide  
 CC (AAW0450) represents a site present in poly(AD-ribose) that is cleaved  
 CC by an ICE-like protein during apoptosis. The 2 peptides were used to test  
 CC the activity of human CPP32, ICE and 2 isoforms, alpha (see also  
 CC AAW06245) and beta (AAW06245), of novel human apoptotic cysteine protease  
 CC Mch2. Enzymatic activities were studied in total bacterial extracts from  
 CC cells expressing these enzymes as GST fusion proteins. Neither Mch2 alpha  
 CC nor Mch2 beta was able to cleave the YVAD substrate. Mch2 alpha, but not  
 CC Mch2 beta, cleaved the DEVD substrate, but was 150-fold less active than  
 CC CPP32.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YYAD 4

PI Kamens J, Allen H, Paskind M, Mankovich JA, Talianian RV;  
 PI Ghayur T;  
 XX WPI; 1996-402371/40.  
 DR Isolated Ich-2 cysteine protease, or fragment - may be used to stimulate  
 XX apoptosis in cells for research purposes.  
 PT

Db 1 YVAD 4

RESULT 11  
AAW45979 ID AAW45979 standard; peptide; 4 AA.  
XX AC AAW45979;  
XX DT 01-JUL-1998 (first entry)DE Cysteine protease inhibiting peptide for preventing cell death.  
XX KW Neuronal cell death; neurodegenerative disorder; inhibition;  
KW cysteine protease; cardiovascular; liver disease.  
XX OS Synthetic.  
XX PN WO9735876-A1.  
XX PD 02-OCT-1997.  
XX PR 04-MAR-1997; 97WO-US004158.  
XX PR 04-MAR-1996; 96US-00010220.  
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.  
PI Troy CM;DR 1997-489561/45.  
PS Disclosure; Page 64; 112pp; English.  
XX This sequence is shown in the specification. The invention relates to peptides of the formula:  $V-(AA1)n-Cys(V')-(AA2)m-V-$  (I), in which n and m = 0-5, totalling 5; if n = 1, AA1 = AA; X = any amino acid; P = Gin-Ala; and if n = 3 or more, (AA1)n = (X)p-Gin-AA; X = any amino acid; P = 1-3, depending on value of n; if m = 1, AA2 = Arg; if m = 2, (AA2)n = Arg-Gly; if m = 3 or more, (AA2)n = Arg-Gly-(X)Q; Q = 1-3, depending on value of m; V, V', and V'', any or all of which may be absent, = agent able to direct the compound to a specific cell. The peptides are inhibitors of cysteine proteases, specifically interleukin-1-beta converting enzyme (ICE). They inhibit death of cells, particularly in humans, and can be used to treat neurodegenerative diseases (e.g. ageing, Alzheimer's, Machado-Joseph, Parkinson's or Huntington's diseases, multiple sclerosis, muscular dystrophy, stroke), cardiovascular disease and liver disorders. The peptides should be more specific than pseudosubstrate inhibitors

SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4

Db 1 YVAD 4

RESULT 12  
AAW7199 ID AAW76199 standard; protein; 4 AA.  
XX AC AAW76199;  
XX DT 26-NOV-1998 (first entry)Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4

Db 1 YVAD 4

RESULT 13  
AAW52749 ID AAW52749 standard; peptide; 4 AA.

XX AC AAW52749;

XX DT 02-MAR-1999 (first entry)

XX DE Aminomethylcoumarin-substituted tetrapeptide.

XX KW Aminomethylcoumarin; fluorescent; interleukin; ICE; caspase;

XX OS Synthetic.

XX PH Location/Qualifiers

Key 1  
PT Modified-site  
PT /note= "the N-terminal is acetylated"

PT Modified-site 4 /note= "the C-terminal is condensed onto 7-amino- 4-  
 PT methyl-coumarin via an amide linkage"  
 XX GB2324529-A.  
 PN XX  
 PD 28-OCT-1998.  
 XX PF 20-FEB-1998; 98GB-00003559.  
 XX PR 21-FEB-1997; 97US-0038656P.  
 XX PA (MERCK ) MERCK & CO INC.  
 XX PI Chapman KR, Nicholson D, Rano T, Thornberry N;  
 DR ;  
 XX DR ;  
 XX PT New tetrapeptide coumarin derivatives - useful in combinatorial libraries  
 PT to identify substrate specificity of cysteine or serine proteases e.g.  
 PT interleukin-1 converting enzyme.  
 XX Claim 3; Page 40; 49pp; English.  
 PS XX

The peptide is a specifically claimed example of new aminomethyl-coumarin-labelled tetrapeptides of formula Ac-Xaa-Xaa-Xaa-Asp-AMC. The tetrapeptides are used to generate a fluorescent positional scanning synthetic combinatorial library for the investigation of the substrate specificity of cysteine and serine proteases e.g. in the analysis of interleukin-1 beta converting enzyme substrate and other caspase substrates, and to identify inhibitors which may mediate inflammations. The library preferably comprises a mixture of at least 200 of the tetrapeptides.

XX Sequence 4 AA;  
 CC Query Match 100.0%; Score 21; DB 2; Length 4;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC AC AAW5304 standard; peptide; 4 AA.  
 CC XX  
 CC DT 22-JUL-1998 (first entry)  
 CC DB Peptide cleaved by interleukin-1-beta-converting enzyme-like protein.  
 CC XX  
 CC N-acetyl-YYAD-methyl coumarinamide; MCA;  
 CC interleukin-1- beta converting enzyme-like activity; ICE activity.  
 CC OS Synthetic.  
 CC XX  
 CC PN JP10099075-A.  
 CC XX  
 CC DT 21-APR-1998.  
 CC DE XX  
 CC PF 30-SEP-1996; 96JUP-00276813.  
 CC XX  
 CC PR 30-SEP-1996; 96JUP-00276813.  
 CC PA (SHISEIDO CO LTD.  
 CC XX  
 CC DR ;  
 CC WPI; 1998-289868/26.

XX Key Location/Qualifiers  
 PT Modified-site 1 /note= "N-terminal acetylation"  
 PT Modified-site 4 /note= "C-terminal Asp-PNA"  
 XX WO9816505-A1.  
 PN XX  
 PD 23-APR-1998.  
 XX XX  
 PF 09-OCT-1997; 97WO-US018396.  
 XX XX

PR 11-OCT-1996; 96JUS-0028313P.  
 XX PA (WARNER LAMBERT CO.  
 XX PI Albrecht HP, Alien HJ, Brady KD, Harter WG, Kostlan CR, Roth BD,  
 PI Walker N;  
 XX DR ;  
 XX WPI; 1998-31002/27.  
 XX PT New sulphonamide compounds - are inhibitors of interleukin-1beta  
 PT converting enzyme and caspase-4, used for treating stroke and  
 PT inflammatory diseases, etc.  
 XX PS Example 6; Page 35; 5pp; English.  
 XX The invention provides sulphonamide compounds of specified formula and  
 CC their salts, esters, anides and prodrugs. The sulphonamide compounds are  
 CC used for inhibiting interleukin 1beta converting enzyme (ICE), inhibiting  
 CC caspase-4, treating or preventing stroke, inflammatory diseases e.g.  
 CC arthritis, inflammatory bowel disease, septic shock, reperfusion injury,  
 CC Alzheimer's disease and shigellosis. The present sequence represents a  
 CC peptide substrate specific for ICE  
 XX Sequence 4 AA;  
 CC Query Match 100.0%; Score 21; DB 2; Length 4;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC AC AAW5304 standard; peptide; 4 AA.  
 CC XX  
 CC DT 22-JUL-1998 (first entry)  
 CC DB Peptide cleaved by interleukin-1-beta-converting enzyme-like protein.  
 CC XX  
 CC N-acetyl-YYAD-methyl coumarinamide; MCA;  
 CC interleukin-1- beta converting enzyme-like activity; ICE activity.  
 CC OS Synthetic.  
 CC XX  
 CC PN JP10099075-A.  
 CC XX  
 CC DT 21-APR-1998.  
 CC DE XX  
 CC PF 30-SEP-1996; 96JUP-00276813.  
 CC XX  
 CC PR 30-SEP-1996; 96JUP-00276813.  
 CC PA (SHISEIDO CO LTD.  
 CC XX  
 CC DR ;  
 CC WPI; 1998-289868/26.

XX Protein with interleukin-1-beta converting enzyme-like activity - useful  
 PT in investigation of substrate specificity in, e.g. Parkinson's disease.  
 XX PS Disclosure; Page 2; 5pp; Japanese.  
 XX The present sequence, N-acetyl-YYAD-methyl coumarinamide (MCA),  
 CC represents a sequence that is cleaved by a protein with interleukin-1-  
 CC beta converting enzyme (ICE)-like activity. The protein, which is  
 CC obtained from human keratinocytes, has a relative molecular weight of 80  
 CC kDa. The ICE protein is part of the cysteine protease family and is  
 CC useful for investigation of the mechanism of substrate specificity (e.g.

CC Alzheimer's disease, Parkinson's disease, autoimmune disease, lymphoma,  
CC cancer and apoptosis)  
XX  
SQ Sequence 4 AA;  
Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YVAD 4  
| |||  
Db 1 YVAD 4

Search completed: May 24, 2004, 14:38:15  
Job time : 53 secs

GenCore version 5.1.6  
(c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: May 24, 2004, 14:36:17 ; Search time 16.5 Seconds  
(without alignments)

12.515 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	21	100.0	4	1	US-08-354-685-1	Sequence 1, Appli	Sequence 1, Appli
2	21	100.0	4	1	US-08-446-925-10	Sequence 10, Appli	Sequence 10, Appli
3	21	100.0	4	1	US-08-446-944-1	Sequence 1, Appli	Sequence 2, Appli
4	21	100.0	4	1	US-08-446-944-2	Sequence 2, Appli	Sequence 16, Appli
5	21	100.0	4	1	US-08-700-716-1	Sequence 16, Appli	Sequence 4, Appli
6	21	100.0	4	1	US-08-592-0-9-4	Sequence 5, Appli	Sequence 8, Appli
7	21	100.0	4	1	US-08-592-0-9-5	Sequence 11, Appli	Sequence 11, Appli
8	21	100.0	4	1	US-08-592-0-9-6	Sequence 16, Appli	Sequence 16, Appli
9	21	100.0	4	1	US-08-592-0-9-7	Sequence 16, Appli	Sequence 16, Appli
10	21	100.0	4	2	US-08-800-007A-11	Sequence 17, Appli	Sequence 17, Appli
11	21	100.0	4	2	US-08-440-898-1	Sequence 1, Appli	Sequence 1, Appli
12	21	100.0	4	2	US-08-440-898-2	Sequence 1, Appli	Sequence 1, Appli
13	21	100.0	4	2	US-09-067-053-1	Sequence 2, Appli	Sequence 2, Appli
14	21	100.0	4	2	US-09-146-3-11-16	Sequence 4, Appli	Sequence 4, Appli
15	21	100.0	4	2	US-08-394-189B-16	Sequence 10, Appli	Sequence 10, Appli
16	21	100.0	4	2	US-08-394-189B-17	Sequence 16, Appli	Sequence 16, Appli
17	21	100.0	4	2	US-08-828-941A-1	Sequence 1, Appli	Sequence 1, Appli
18	21	100.0	4	2	US-08-828-941A-2	Sequence 2, Appli	Sequence 2, Appli
19	21	100.0	4	2	US-08-883-632-4	Sequence 4, Appli	Sequence 4, Appli
20	21	100.0	4	2	US-08-883-632-5	Sequence 5, Appli	Sequence 5, Appli
21	21	100.0	4	2	US-08-915-114A-4	Sequence 2, Appli	Sequence 2, Appli
22	21	100.0	4	2	US-08-592-013A-4	Sequence 4, Appli	Sequence 4, Appli
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25	21	100.0	4	2	US-08-712-878-1	Sequence 1, Appli	Sequence 1, Appli
26	21	100.0	4	2	US-08-712-878-8	Sequence 8, Appli	Sequence 8, Appli
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RESULT 1  
US-08-54-685-1  
Sequence 1, Application US/08354685  
Patent No. 5493695  
GENERAL INFORMATION:  
APPLICANT: Dauny, Gaston O.  
APPLICANT: Reiter, Lawrence A.  
TITLE OF INVENTION: PARA-NITROANILIDE PEPTIDES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSSEE: Dr. Peter C. Richardson  
STREET: 235 East 42nd Street, 20th Floor  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10017-5755  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/354,685  
FILING DATE: 2001-07-17  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 981,153  
FILING DATE: 24-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stassburger, Philip C.  
REGISTRATION NUMBER: 34,258  
REFERENCE/DOCKET NUMBER: PC8352  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 573-5731  
TELEFAX: (212) 573-1939  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
SEQUENCE LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
LENGTH: 4 amino acids

Query Match Similarity 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YVAD 4

Db 1 YVAD 4

RESULT 2

US-08-446-925-10

Sequence 10, Application US/08446925

Patent No. 5,672,500

GENERAL INFORMATION:

APPLICANT: Litwack, Gerald

APPLICANT: Fernandez-Almendri, Teresa

TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE

TITLE OF INVENTION: PROTEASE,

TITLE OF INVENTION: AND COMPOSITIONS FOR MAKING AND

TITLE OF INVENTION: METHODS

TITLE OF INVENTION: OF USING THE SAME

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &amp;

ADDRESSEE: No. 5672500ris

STREET: One Liberty Place, 46th floor

CITY: Philadelphia

STATE: PA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,925

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: DeLuca, Mark

REGISTRATION NUMBER: 33,229

SEQUENCE DOCKET NUMBER: TUTU-1508

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-4339

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

CLASSIFICATION: 536

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /product= "OTHER"

OTHER INFORMATION: 1 /product= "OTHER"

OTHER INFORMATION: /note= "tyrosine is succinylated"

FEATURE: /note= "p-nitroanilide"

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /product= "OTHER"

OTHER INFORMATION: 1 /product= "OTHER"

OTHER INFORMATION: /note= "aspartic acid residue is derivatized with

US-08-464-964-1

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4

Db 1 YVAD 4

RESULT 3

US-08-464-964-1

Sequence 1, Application US/08464964

Patent No. 5,716,929

GENERAL INFORMATION:

APPLICANT: Bemis, Guy W.

APPLICANT: Golec, Julian M.C.

APPLICANT: Lauffer, David J.

APPLICANT: Mullican, Michael D

APPLICANT: Murcko, Mark A

APPLICANT: Livingston, David J.

TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1 BETA

TITLE OF INVENTION: CONVERTING ENZYME

NUMBER OF SEQUENCES: 2

|||||  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr.  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10020  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/464,964  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/261,452  
 FILING DATE: 17-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haley Jr., James F.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: VPI/94-04 CIPPI DIVI  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-596-9000  
 TELEFAX: 212-596-9090  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 1  
 OTHER INFORMATION: /product= "OTHER"  
 OTHER INFORMATION: 1 /product= "OTHER"  
 OTHER INFORMATION: /note= "tyrosine is succinylated"  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 4  
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 OTHER INFORMATION: 1 /product= "OTHER"  
 OTHER INFORMATION: /note= "aspartic acid residue is derivatized with  
 US-08-464-964-1  
 Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YVAD 4  
 Db 1 YVAD 4  
 RESULT 4  
 US-08-464-964-2  
 Sequence 2, Application US/08464964  
 Patents No. 5,716,929  
 GENERAL INFORMATION:  
 APPLICANT: Lauffer, David J.  
 APPLICANT: Bemis, Guy W.  
 APPLICANT: Golec, Julian M.C.  
 APPLICANT: Livingston, David J.  
 APPLICANT: Mullican, Michael D  
 APPLICANT: Murcko, Mark A

APPLICANT: Livingston, David J  
 TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1 BETA  
 TITLE OF INVENTION: CONVERTING ENZYME  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr.  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10020  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/Ms-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/464,964  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/440,898  
 FILING DATE: 25-MAY-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/405,581  
 FILING DATE: 17-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/261,452  
 FILING DATE: 17-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haley Jr., James F.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: VPI/94-04 CIPII DIVI  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-596-9000  
 TELEFAX: 212-596-9090  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
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 LOCATION: 4  
 OTHER INFORMATION: /product= "OTHER"  
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 LOCATION: 4  
 OTHER INFORMATION: /product= "aspartic acid is derivatized"  
 OTHER INFORMATION: amino-4-methylcoumarin"  
 US-08-464-964-2

Query Match 100.0%; Score 21; DB 1; Length 5  
 Best local Similarity 100.0%; Prod. No. 3e+05; Mismatches 0; Indels 0

Qy	1 YYAD 4
Db	1 YYAD 4

RESULT 5  
 US-08-700-716-1  
 Sequence 1, Application US/08700716  
 Patent No. 574451  
 GENERAL INFORMATION:  
 APPLICANT: Allen, Hamish J

```

APPLICANT: Banerjee, Subhashis
APPLICANT: Brady, Kenneth D
APPLICANT: Hodges, John C
APPLICANT: Kostlan, Catherine R
APPLICANT: Talianian, Robert V
TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Elizabeth M. Anderson
STREET: 2800 Plymouth Road
CITY: Ann Arbor
STATE: MI
COUNTRY: US
ZIP: 48105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver 1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,716
FILING DATE: 13-AUG-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION
NAME: Anderson, Elizabeth M
REGISTRATION NUMBER: 31185
REFERENCE/DOCKET NUMBER: PD-5363-01-EMA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313 996-7304
TELEFAX: 313 996-1553
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-700-716-1

Query Match 100.0% Score 21; DB 1; Length 4;
Best Local Similarity 100.0% Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Dy |||||
Db 1 YVAD 4

RESULT 6
US-08-700-716-16
Sequence 16, Application US/08700716
Patent No. 5744451
GENERAL INFORMATION:
APPLICANT: Allen, Hamish J
APPLICANT: Banerjee, Subhashis
APPLICANT: Brady, Kenneth D
APPLICANT: Hodges, John C
APPLICANT: Kostlan, Catherine R
APPLICANT: Talianian, Robert V
TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Elizabeth M. Anderson
STREET: 2800 Plymouth Road
CITY: Ann Arbor
STATE: MI
COUNTRY: US
ZIP: 48105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Ver 1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/700,716  
 FILING DATE: 13-AUG-1996  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Anderson, Elizabeth M  
 REGISTRATION NUMBER: 31:85  
 REFERENCE/DOCKET NUMBER: PD-5363-01-EMA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 313 996-7304  
 TELEFAX: 313 996-1553  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-700-716-16

Query Match Best Local Similarity 100.0%; Score 21; DB 1; Length 4;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
 Db 1 YVAD 4

RESULT 7  
 US-08-592-029-4  
 Sequence 4, Application US/08592029  
 / Patent No. 5763196  
 / GENERAL INFORMATION:  
 / APPLICANT: POWELL, MICHAEL J.  
 / APPLICANT: KHANNA, PYARE  
 / APPLICANT: LINGENFELTER, DAVID  
 / APPLICANT: EISENBEIS, SCOTT J.  
 / TITLE OF INVENTION: ASSAYS USING CROSS-LINKED POLYPEPTIDE  
 / NUMBER OF SEQUENCES: 9  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: MORRISON & FOERSTER  
 / STREET: 755 PAGE MILL ROAD  
 / CITY: PALO ALTO  
 / STATE: CA  
 / COUNTRY: USA  
 / ZIP: 94304-1018  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/592,029  
 / FILING DATE: 26-JAN-1996  
 / CLASSIFICATION: 435  
 / COMPUTER READABLE FORM: Floppy disk  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patentin Release #1.0, Version #1.30  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/592,029  
 / FILING DATE: 26-JAN-1996  
 / CLASSIFICATION: 35  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: MONROY, GLADYS H.  
 / REGISTRATION NUMBER: 32,430  
 / REFERENCE/DOCKET NUMBER: 33746-20004.00  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (415) 813-5600  
 / TELEFAX: (415) 494-0792  
 / TELEX: 70641 MRSNFORS SFO  
 / INFORMATION FOR SEQ ID NO: 4:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 4 amino acids  
 / TYPE: amino acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear

FEATURE: Modified-site  
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 US-08-592-029-4  

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 Db 1 YVAD 4

RESULT 8  
 US-08-592-029-5  
 Sequence 5, Application US/08592029  
 / Patent No. 5763196  
 / GENERAL INFORMATION:  
 / APPLICANT: POWELL, MICHAEL J.  
 / APPLICANT: KHANNA, PYARE  
 / APPLICANT: LINGENFELTER, DAVID  
 / APPLICANT: EISENBEIS, SCOTT J.  
 / TITLE OF INVENTION: ASSAYS USING CROSS-LINKED POLYPEPTIDE  
 / NUMBER OF SEQUENCES: 9  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: MORRISON & FOERSTER  
 / STREET: 755 PAGE MILL ROAD  
 / CITY: PALO ALTO  
 / STATE: CA  
 / COUNTRY: USA  
 / ZIP: 94304-1018  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patentin Release #1.0, Version #1.30  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/592,029  
 / FILING DATE: 26-JAN-1996  
 / CLASSIFICATION: 435  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: MONROY, GLADYS H.  
 / REGISTRATION NUMBER: 32,430  
 / REFERENCE/DOCKET NUMBER: 33746-20004.00  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (415) 813-5600  
 / TELEFAX: (415) 494-0792  
 / TELEX: 70641 MRSNFORS SFO  
 / INFORMATION FOR SEQ ID NO: 5:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 4 amino acids  
 / TYPE: amino acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear

OTHER INFORMATION: /product= "OTHER"  
 OTHER INFORMATION: /label= "Ac-Tyr/  
 /note= "Acetyl tyrosine"  
 US-08-592-029-5

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Qy 1 YVAD 4  
 Db 1 YVAD 4

RESULT 9  
 US-08-777-208-8  
 Sequence 8, Application US/08777208  
 Patent No. 573576

GENERAL INFORMATION:  
 APPLICANT: Powers, James C.  
 TITLE OF INVENTION: Tetrapeptide Alpha-Ketoamides  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Deveau, Colton & Marquis  
 STREET: Two Midtown Plaza, Suite 1400  
 CITY: Atlanta  
 STATE: GA  
 COUNTRY: USA  
 ZIP: 30309

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Microsoft Windows 95  
 SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/777,208  
 FILING DATE: 27-DEC-1996  
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/539944  
 FILING DATE: 06-OCT-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Colton, Laurence P.  
 REGISTRATION NUMBER: 33371  
 REFERENCE/DOCKET NUMBER: 10733-191B

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404) 875-3555  
 TELEFAX: (404) 875-8505

INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: no

US-08-777-208-8

APPLICANT: Rotonda, Jennifer  
 APPLICANT: Thornberry, Nancy  
 APPLICANT: Fazil, Kimberly  
 APPLICANT: Gallant, Michel  
 APPLICANT: Gareau, Yves  
 APPLICANT: Labelle, Marc  
 APPLICANT: Peterson, Brin  
 APPLICANT: Rasper, Diana  
 TITLE OF INVENTION: CRYSTAL STRUCTURE OF APOBAIN  
 TITLE OF INVENTION: AND USES THEREOF  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: JOSEPH A. COPPOLA - MERCK & CO., INC.  
 STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
 CITY: Rahway  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 07065

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ FOR WINDOWS Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/000,007A  
 FILING DATE: 13-FEB-1997  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: COPPOLA, JOSEPH A.  
 REGISTRATION NUMBER: 38,413  
 REFERENCE/DOCKET NUMBER: 19644  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 732-594-6734  
 TELEFAX: 732-594-4720  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-800-007A-11

Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
 Db 1 YVAD 4

RESULT 11  
 US-08-440-898-1  
 Sequence 11, Application US/08440898  
 Patent No. 5847135

GENERAL INFORMATION:  
 APPLICANT: Benis, Guy W.  
 APPLICANT: Golec, Julian M.C.  
 APPLICANT: Laufer, David J.  
 APPLICANT: Mulligan, Michael D  
 APPLICANT: Murcko, Mark A.  
 APPLICANT: Livingston, David J.  
 TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1  
 NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr.  
 STREET: 1251 Avenue of the Americas

CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10020  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/440,898  
 FILING DATE: 25-MAY-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/405,581  
 FILING DATE: 17-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/261,452  
 FILING DATE: 17-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haley Jr., James F.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: VPI/94-04 CIPPI DIVI  
 TELECOMMUNICATION INFORMATION  
 TELEPHONE: 212-596-9000  
 TELEFAX: 212-596-0090  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
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 S-08-440-898-1

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 Matches 4; Conservative 0; Mismatches 0;

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S-08-440-898-2  
 Sequence 2, Application US/08440898  
 Patent No. 584735

GENERAL INFORMATION:  
 APPLICANT: Bemis, Guy W.  
 APPLICANT: Golec, Julian M.C.  
 APPLICANT: Laufer, David J.  
 APPLICANT: Mulligan, Michael D.  
 APPLICANT: Murcko, Mark A.  
 APPLICANT: Livingston, David J.  
 TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1  
 TITLE OF INVENTION: BETA CONVERTING ENZYME  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr.

STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10020  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version 1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/440,898  
 FILING DATE: 25-MAY-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08 / 405,581  
 FILING DATE: 17-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08 / 261,452  
 FILING DATE: 17-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haley Jr., James F.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: VPI/94-04  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-596-9000  
 TELEFAX: 212-596-0900  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI -SENSE: NO  
 FEATURE:  
 NAME/KEY: Modified-site  
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 Matches 4; Conservative 0; Mismat  
 Qy 1 YVAD 4  
 Ddb 1 YVAD 4

ADDRESSEE: Elizabeth M. Anderson  
 STREET: 2800 Plymouth Road  
 CITY: Ann Arbor  
 STATE: MI  
 COUNTRY: US  
 ZIP: 48105

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Ver 1.36  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/067,053  
 FILING DATE: 27-APR-1998

CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Anderson, Elizabeth M  
 REGISTRATION NUMBER: 31585  
 REFERENCE/DOCKET NUMBER: PD-5363-01-EMA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 313 996-1553  
 TELEX/FAX: 313 996-7304

INFORMATION FOR SEQ ID NO: 1  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 STRAND: 1  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

US-09-067-053-1

Query Match Similarity 100.0%; Pred. No. 3e-05;  
 Best Local Similarity 100.0%; Pred. No. 3e-05;  
 Matches 4; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 YVAD 4

Db 1 YVAD 4

Query Match Similarity 100.0%; Pred. No. 3e-05;  
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 Matches 4; Conservative 0; Mismatches 0;  
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Qy 1 YVAD 4

Db 1 YVAD 4

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 Best Local Similarity 100.0%; Pred. No. 3e-05;  
 Matches 4; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 YVAD 4

Db 1 YVAD 4

RESULT 14  
 US-09-067-053-16  
 Sequence 16, Application US/09067053  
 GENERAL INFORMATION:  
 APPLICANT: Allen, Hamish J  
 APPLICANT: Banerjee, Subhashis  
 APPLICANT: Brady, Kenneth D  
 APPLICANT: Hodges, John C  
 APPLICANT: Koslani, Catherine R  
 APPLICANT: Talarian, Robert V  
 TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Elizabeth M. Anderson  
 STREET: 2800 Plymouth Road  
 CITY: Ann Arbor  
 STATE: MI  
 COUNTRY: US  
 ZIP: 48105

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Ver 1.36  
 CURRENT APPLICATION DATA:  
 REFERENCE/DOCKET NUMBER: PD-5363-01-EMA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEX/FAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 10  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid

; - TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-146-31-10  
Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. NO. 3e-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YYAD 4  
Db 1 YYAD 4

Search completed: May 24, 2004, 14:38:59  
Job time : 16.5 secs

GenCore version 5.1.6  
Copyright (C) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2004, 14:39:37 : Search time 38 Seconds

(without alignments)  
29.360 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 114331 seqs, 278921704 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications AA:\*

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#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	21	100.0	4 9 US-09-799-463-3	Sequence 3, Appli
3	21	100.0	4 9 US-09-735-163A-84	Sequence 8, Appli
4	21	100.0	4 9 US-09-799-994-3	Sequence 3, Appli
5	21	100.0	4 9 US-09-952-768-72	Sequence 72, Appli
6	21	100.0	4 9 US-09-150-23-7	Sequence 7, Appli
7	21	100.0	4 9 US-09-858-754-10	Sequence 10, Appli
8	21	100.0	4 9 US-09-987-417-2	Sequence 2, Appli
9	21	100.0	4 9 US-09-977-831-35	Sequence 35, Appli
10	21	100.0	4 9 US-09-888-143-17	Sequence 17, Appli
11	21	100.0	4 9 US-09-947-187-2	Sequence 2, Appli
12	21	100.0	4 9 US-09-964-114-3	Sequence 3, Appli
13	21	100.0	4 9 US-09-164-114-4	Sequence 4, Appli
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COUNTRY: New York

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA: US/08/610-220A

FILING DATE: MAR-04-1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28, 678

REFERENCE/DOCKET NUMBER: 48332/JPM/JML

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400

TELEFAX: 212-311-0525

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

RESULT 1  
US-09-610-220A-7  
Sequence 7, Application US/08/610-220A  
Publication No. US2003039638A1  
GENERAL INFORMATION:  
APPLICANT: Troy, Carol M.

TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL DEATH AND USES THEREOF  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York

ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.

REGISTRATION NUMBER: 28, 678  
REFERENCE/DOCKET NUMBER: 48332/JPM/JML

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-311-0525

SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

#### ALIGNMENTS

MOLECULE TYPE: Peptide  
 US-08-610-220A-7  
 Query Match 100.0%; Score 21; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 Db 1 YVAD 4

RESULT 2  
 US-09-793-463-3  
 Sequence 3, Application US/09799463  
 Patent No. US20010018195A1  
 GENERAL INFORMATION:  
 APPLICANT: Reed, John C.  
 APPLICANT: Deveraux, Quinn  
 APPLICANT: Salvesen, Guy S.  
 APPLICANT: Takahashi, Ryosuke  
 APPLICANT: Roy, Natalie  
 TITLE OF INVENTION: Apoptosis (IAP) Protein Regulation of Caspase Activity  
 FILE REFERENCE: LJ 3800  
 CURRENT APPLICATION NUMBER: US/09/799, 994  
 CURRENT FILING DATE: 2001-03-05  
 PRIOR APPLICATION NUMBER: 09/0058, 969  
 PRIOR FILING DATE: 1998-04-10  
 PRIOR APPLICATION NUMBER: 08/862, 087  
 PRIOR FILING DATE: 1997-05-22  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 3  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Unknown  
 FEATURE:  
 OTHER INFORMATION: Description of Unknown Organism:Consensus Sequence

US-09-793-463-3  
 OTHER INFORMATION: Description of Unknown Organism:Consensus Sequence

Query Match 100.0%; Score 21; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
 Db 1 YVAD 4

RESULT 3  
 US-09-735-363A-84  
 Sequence 84, Application US/09735363A  
 Patent No. US20010041681A1  
 GENERAL INFORMATION:  
 APPLICANT: Pillion, Mario  
 APPLICANT: Phillip, Nigel  
 TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
 FILE REFERENCE: 02811-0181  
 CURRENT APPLICATION NUMBER: US/09/735, 363A  
 CURRENT FILING DATE: 2000-12-12  
 PRIOR APPLICATION NUMBER: 60/170, 325  
 PRIOR FILING DATE: 1999-12-13  
 PRIOR APPLICATION NUMBER: 60/228, 925  
 PRIOR FILING DATE: 2000-08-29  
 NUMBER OF SEQ ID NOS: 87  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 84  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic Peptide

US-09-735-363A-84  
 Query Match 100.0%; Score 21; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 Db 1 YVAD 4

RESULT 4  
 US-09-799-994-3  
 Sequence 3, Application US/09799994  
 Patent No. US20020000957A1  
 GENERAL INFORMATION:  
 APPLICANT: Reed, John C.  
 APPLICANT: Deveraux, Quinn  
 APPLICANT: Salvesen, Guy S.  
 APPLICANT: Roy, Natalie  
 APPLICANT: Takahashi, Ryosuke  
 TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor Of Caspase Activity  
 FILE REFERENCE: LJ 3800  
 CURRENT APPLICATION NUMBER: US/09/799, 994  
 CURRENT FILING DATE: 2001-03-05  
 PRIOR APPLICATION NUMBER: 09/058, 969  
 PRIOR FILING DATE: 1998-04-10  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 3  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Unknown  
 FEATURE:  
 OTHER INFORMATION: Description of Unknown Organism:Consensus Sequence

US-09-799-994-3  
 Query Match 100.0%; Score 21; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 Db 1 YVAD 4

RESULT 5  
 US-09-952-768-72  
 Sequence 72, Application US/09932768  
 Patent No. US20020035242A1  
 GENERAL INFORMATION:  
 APPLICANT: Almeirai, Emad S.  
 APPLICANT: Fernandes-Almeirai, Teresa  
 APPLICANT: Armstrong, Robert  
 APPLICANT: Tomazelli, Kevin  
 TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE, NUCLEAR ACIDS ENCODING AND METHODS OF USE  
 NUMBER OF SEQUENCES: 75  
 CORRESPONDENCE ADDRESS:  
 STREET: Seed Intellectual Property Law Group  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952,768  
 FILING DATE: 10-Sep-2001  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Christiansen, William T.  
 REGISTRATION NUMBER: 44,614  
 REFERENCE/DOCKET NUMBER: 480140.424C4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-0300  
 INFORMATION FOR SEQ ID NO: 72:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acid  
 TYPE: amino acid  
 STRANDEDNESS: <Unknown>  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
 US-09-952-768-72

Query Match 100.0%; Score 21; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4  
 Db 1 YYAD 4

RESULT 6  
 US-09-150-023-7  
 Sequence 7, Application US/09150623  
 Patent No. US2002004491A1  
 GENERAL INFORMATION:  
 APPLICANT: TROY, Carol M.  
 TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL  
 NUMBER OF SEQUENCES: 11  
 TITLE OF INVENTION: DEATH AND USES THEREOF  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/150,623  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/610,220  
 FILING DATE: MAR-04-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 43332/JPW/JML  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-278-0400  
 TELEFAX: 212-391-0525  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acid  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-150-623-7

Query Match 100.0%; Score 21; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4  
 Db 1 YYAD 4

RESULT 7  
 US-09-858-754-10  
 Sequence 10, Application US/09858754  
 Patent No. US20020055130A1  
 GENERAL INFORMATION:  
 APPLICANT: Johnson, Gary L.  
 TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS  
 CURRENT APPLICATION NUMBER: US/09/858,754  
 CURRENT FILING DATE: 2001-05-16  
 PRIOR APPLICATION NUMBER: 09/023,130  
 PRIOR FILING DATE: 1998-02-13  
 PRIOR APPLICATION NUMBER: 60/039,740  
 PRIOR FILING DATE: 1997-02-14  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 10  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: synthetic construct  
 US-09-858-754-10

Query Match 100.0%; Score 21; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4  
 Db 1 YYAD 4

RESULT 8  
 US-09-987-417-2  
 Sequence 2, Application US/09987417  
 Patent No. US2002005631A1  
 GENERAL INFORMATION:  
 APPLICANT: Cai, Sui Xiong  
 APPLICANT: Weber, Eckard  
 APPLICANT: Wang, Yan  
 APPLICANT: Mills, Gordon B.  
 APPLICANT: Green, Douglas R.  
 TITLE OF INVENTION: Caspase Inhibitors and the Use Thereof  
 FILE REFERENCE: 1735-0350003  
 CURRENT APPLICATION NUMBER: US/09/987,417  
 CURRENT FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 09/545,565  
 PRIOR FILING DATE: 2000-04-07  
 PRIOR APPLICATION NUMBER: US 60/128,545  
 PRIOR FILING DATE: 1999-04-09  
 PRIOR APPLICATION NUMBER: US 60/158,370  
 PRIOR FILING DATE: 1999-10-12  
 NUMBER OF SEQ ID NOS: 3  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 2  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Unknown Organism  
 FEATURE:  
 OTHER INFORMATION: caspase-1 inhibitor  
 US-09-987-417-2

Query Match 100.0%; Score 21; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;







ORGANISM: Unknown Organism  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: caspase-1  
PCT-US01-093-2

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 3  
SOFTWARE: PatentIn Ver. 2.1

Db 1 YVAD 4

RESULT 4  
PCT-US02-18014-9  
Sequence 9, Application PC/TUS0218014  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation

APPLICANT: Rechsteiner Martin  
APPLICANT: Pratt, Gregory  
TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS WITH  
TITLE OF INVENTION: THERAPEUTIC POTENTIAL FOR TREATMENT OF CENTRAL  
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES RESULTING FROM ABNORMAL PROTEIN  
TITLE OF INVENTION: OR PEPTIDE ACCUMULATION

FILE REFERENCE: 21101.0013P1  
CURRENT APPLICATION NUMBER: PCT/US02/18014  
CURRENT FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: 60/297,332

PRIOR FILING DATE: 2001-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9  
LENGTH: 4

TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Caspase

Qy 1 YVAD 4  
Db 1 YVAD 4

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 9  
LENGTH: 4

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Caspase

PCT-US01-04137-2  
Sequence 3, Application PC/TUS0104137  
GENERAL INFORMATION:  
APPLICANT: ALEXION PHARMACEUTICALS, INC.

APPLICANT: Fodor, William L.

TITLE OF INVENTION: MIXTURES OF CASPASE INHIBITORS AND COMPLEMENT

FILE REFERENCE: 108715PCT

CURRENT APPLICATION NUMBER: PCT/US01/04137

CURRENT FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9  
LENGTH: 4

TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Synthetic peptide

NAME/KEY: MOD-RES  
LOCATION: (1) .. (1)

OTHER INFORMATION: Benzoyl carbonyl moiety

NAME/KEY: MOD-RES  
LOCATION: (4) .. (4)

OTHER INFORMATION: 7-amino-4-trifluoromethylcoumarin

PCT-US02-18484-9

Qy 1 YVAD 4

Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO 7

Length: 4  
 TYPE: PRT  
 ORGANISM: Artificial  
 FEATURE: Substrate

Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO 7

Length: 4  
 TYPE: PRT  
 ORGANISM: Artificial  
 FEATURE: Substrate

Query 1 YVAD 4  
 Db 1 YVAD 4

RESULT 8  
 PCT-US96-07010-10  
 Sequence 10, Application PC/TUS9607010  
 GENERAL INFORMATION:  
 APPLICANT: Litwick, Gerald  
 APPLICANT: Alnemri, Emad S.  
 APPLICANT: Fernandez-Alnemri, Teresa  
 TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE PROTEASE, AND COMPOSITIONS FOR MAKING AND METHODS OF USING THE  
 TITLE OF INVENTION: SAME  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Woodcock, Blackburn, Kurtz, Mackiewicz &  
 ADDRESSEE: Norris  
 STREET: One Liberty Place, 46th floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/07010  
 FILING DATE: 1995-05-10  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DeLuca, Mark  
 REGISTRATION NUMBER: 33,229  
 REFERENCE/DOCKET NUMBER: TJU-1882  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO 3

Length: 4  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: Synthetic construct

Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO 3

Length: 4  
 TYPE: PRT  
 ORGANISM: Artificial

STREET: 1100 New York Avenue NW, Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US98/12716  
 FILING DATE: Herewith  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 60/050,242  
 FILING DATE: 19-JUN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JOSE A. Goldstein  
 REGISTRATION NUMBER: 29,021  
 REFERENCE/DOCKET NUMBER: 0609.442PC01/JAG/LBB  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 1 OTHER INFORMATION: /product= "OTHER"  
 OTHER INFORMATION: /label= CHO  
 OTHER INFORMATION: /note= "An aldehyde (CHO) is attached to the C-terminal  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 4 OTHER INFORMATION: /product= "OTHER"  
 OTHER INFORMATION: /label= CMK  
 OTHER INFORMATION: /note= "A chloromethylketone (CMK) group is attached to the tyrosine residue."  
 OTHER INFORMATION:  
 PCT-US98-12716-26  
 Query Match Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 10  
 PCT-US98-12716-28  
 Sequence 28, Application PC/TUS9812716  
 GENERAL INFORMATION:  
 APPLICANT: Yuan, Junying  
 APPLICANT: Friedlander, Robert M.  
 TITLE OF INVENTION: Interleukin Converting Enzyme (ICE)  
 NUMBER OF SEQUENCES: 28  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
 STREET: 1100 New York Avenue NW, Suite 600  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

OTHER INFORMATION: Peptide  
PCT-US98-2231-2

Query Match Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YYAD 4  
Db 1 YYAD 4

RESULT 13  
PCT-US99-16423-2

Sequence 36, Application PC/TUS9916423  
GENERAL INFORMATION:  
APPLICANT: Yuan, Junying  
APPLICANT: Morishima, Nobuhiro  
APPLICANT: The General Hospital Corporation  
TITLE OF INVENTION: Programmed Cell Death and Caspase-12  
FILE REFERENCE: 0609-440PC01  
CURRENT FILING DATE: 1999-04-14  
EARLIER APPLICATION NUMBER: US 6,0/081,962  
EARLIER FILING DATE: 1998-04-16  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 36  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide  
PCT-US99-08064-36

Query Match Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YYAD 4  
Db 1 YYAD 4

RESULT 14  
US-08-183-269-1

Query Match Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YYAD 4  
Db 1 YYAD 4

RESULT 14  
US-08-183-269-1

Sequence 1, Application US/08183269  
GENERAL INFORMATION:  
APPLICANT: Molinieux, Susan M.  
APPLICANT: Rolando, Anna M.  
APPLICANT: Casano, Francesca J.  
TITLE OF INVENTION: DNA Encoding Murine Precursor  
TITLE OF INVENTION: Interleukin 1 Beta Converting Enzyme  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/183,269  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/947,330  
FILING DATE: 18-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Wallen, John W.  
REGISTRATION NUMBER: 35,403  
REFERENCE/DOCKET NUMBER: 18857  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3905  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-183-269-1

Query Match Score 21; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YYAD 4  
Db 1 YYAD 4

RESULT 15  
US-08-282-211A-16

Sequence 16, Application US/08282211A  
GENERAL INFORMATION:  
APPLICANT: Horvitz, H. Robert  
APPLICANT: Yuan, Junying  
APPLICANT: Shaham, Shai  
TITLE OF INVENTION: RELATEDNESS OF HUMAN INTERLEUKIN-1  
TITLE OF INVENTION: CONVERTASE GENE TO A C. ELEGANS CELL DEATH GENE  
TITLE OF INVENTION: INHIBITORY PORTIONS OF THESE GENES AND USES THEREFOR  
TITLE OF INVENTION:

```

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2604
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,211A
FILING DATE: 11-JUL-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE DOCKET NUMBER: 01997/198004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-282-211A-16

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Query Match          100.0%;  Score 21;  DB 6;  Length 4;
Best Local Similarity 100.0%;  Fred. No. 5.5e+06;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy      1 YVAD 4
Db      1 YVAD 4

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Search completed: May 24, 2004, 14:47:41  
 Job time : 176 secs



PRIOR FILING DATE: 2003-06-03  
 NUMBER OF SEQ ID NOS: 699  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 528  
 LENGTH: 4  
 TYPE: PRT  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 OTHER INFORMATION: peptide  
 US-10-627-556-528

Query Match Similarity 100.0%; Score 21; DB 6; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Gaps 0;

Qy 1 YVAD 4  
 Db 1 YVAD 4

RESULT 3  
 US-10-630-926-155  
 ; Sequence 15, Application US/10630926  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RICCIARDI, Carlo  
 ; TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
 ; STREET: 624 Ninth Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; ZIP: 20001  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC Compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.1, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/630,926  
 ; FILING DATE: 31-JUL-2003  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/403,861A  
 ; FILING DATE: 11-FEB-2000  
 ; APPLICATION NUMBER: PCT/EP98/02490  
 ; FILING DATE: 27-APR-1998  
 ; APPLICATION NUMBER: EP 97107033,9  
 ; FILING DATE: 28-APR-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: YUN, Allen C.  
 ; REGISTRATION NUMBER: 37,971  
 ; REFEERENCE/DOCKET NUMBER: RICCARDI=1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-377-5297  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FEATURE:  
 ; OTHER INFORMATION: note: "the N-terminus is modified by an  
 ; acetyl group; the C-terminus is modified with CH2OC(O)-[2,6-(CF3)2]Ph"  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
 ; US-10-630-926-155

Query Match Similarity 100.0%; Score 21; DB 6; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
 Db 1 YVAD 4

RESULT 4  
 US-10-829-381-2  
 ; Sequence 2, Application US/10829381  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weber, Eckard  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Keana, John P.W.  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Zhang, Han-Zhong  
 ; TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and Their Applications for Whole-Cell Fluorescence  
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the Use Thereof  
 ; FILE REFERENCE: 1735 0290006  
 ; CURRENT APPLICATION NUMBER: US/10/829,381  
 ; CURRENT FILING DATE: 2004-04-22  
 ; PRIOR APPLICATION NUMBER: US 60/061,582  
 ; PRIOR FILING DATE: 1997-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/145,746  
 ; PRIOR FILING DATE: 1998-03-03  
 ; PRIOR APPLICATION NUMBER: US 09/168,888  
 ; PRIOR FILING DATE: 1998-10-09  
 ; PRIOR APPLICATION NUMBER: US 09/947,387  
 ; PRIOR FILING DATE: 2001-09-07  
 ; NUMBER OF SEQ ID NOS: 142  
 ; SEQ ID NO: 2  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 ; US-10-829-381-2

Query Match Similarity 100.0%; Score 21; DB 6; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
 Db 1 YVAD 4

RESULT 5  
 US-10-665-668A-7  
 ; Sequence 7, Application US/10665668A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TROY, CAROL M.  
 ; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT CELL DEATH AND USES THEREOF  
 ; FILE REFERENCE: 0575/48332-B  
 ; CURRENT APPLICATION NUMBER: US/10/665,668A  
 ; CURRENT FILING DATE: 2003-09-19  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 7  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: MOTIF OF PSEUDOSUBSTRATE INHIBITOR  
 ; US-10-665-668A-7

Query Match Similarity 100.0%; Score 21; DB 6; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
US-10-829-381-72  
Sequence 72, Application US/10829381  
GENERAL INFORMATION:  
APPLICANT: Weber, Eckard  
APPLICANT: Cai, Sui Xiong  
APPLICANT: Keana, John F.W.  
APPLICANT: Drewe, John A.  
APPLICANT: Zhang, Han-Zhong  
TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and Their Applications for Whole-Cell Fluorescence Screening Assays for Caspases and Other Enzymes and the Use Thereof  
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the Use Thereof  
FILE REFERENCE: 1735.0290006  
CURRENT APPLICATION NUMBER: US/10/829,381  
CURRENT FILING DATE: 2004-04-22  
PRIOR APPLICATION NUMBER: US 60/061,582  
PRIOR FILING DATE: 1997-10-10  
PRIOR APPLICATION NUMBER: US 60/145,746  
PRIOR FILING DATE: 1998-03-03  
PRIOR APPLICATION NUMBER: US 09/168,888  
PRIOR FILING DATE: 1998-10-09  
PRIOR APPLICATION NUMBER: US 09/165,888  
PRIOR FILING DATE: 1998-10-09  
PRIOR APPLICATION NUMBER: US 09/947,387  
PRIOR FILING DATE: 2001-09-07  
NUMBER OF SEQ ID NOS: 142  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 72  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
OTHER INFORMATION: Description of Artificial Sequence:Peptide  
US-10-829-381-72  
Query Match 100.0%; Score 21; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;  
Qy 1 YYAD 4  
Db 1 YYAD 4

RESULT 7  
US-10-665-668A-6  
Sequence 6, Application US/10665668A  
GENERAL INFORMATION:  
APPLICANT: TROY, CAROL M.  
TITLE OF INVENTION: COMPOUNDS WHICH PREVENT CELL DEATH AND USES THEREOF  
FILE REFERENCE: 0575/48332-B  
CURRENT APPLICATION NUMBER: US/10/665,668A  
CURRENT FILING DATE: 2003-09-19  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO: 6  
LENGTH: 5  
TYPE: PRT  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: COMPETITIVE INHIBITOR OF ICE  
US-10-665-668A-6  
Query Match 100.0%; Score 21; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;  
Qy 1 YYAD 4

RESULT 8  
US-10-829-381-142  
Sequence 142, Application US/10829381  
GENERAL INFORMATION:  
APPLICANT: Weber, Eckard  
APPLICANT: Cai, Sui Xiong  
APPLICANT: Keana, John F.W.  
APPLICANT: Drewe, John A.  
APPLICANT: Zhang, Han-Zhong  
TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and Their Applications for Whole-Cell Fluorescence Screening Assays for Caspases and Other Enzymes and the Use Thereof  
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the Use Thereof  
FILE REFERENCE: 1735.0290006  
CURRENT APPLICATION NUMBER: US/10/829,381  
CURRENT FILING DATE: 2004-04-22  
PRIOR APPLICATION NUMBER: US 60/061,582  
PRIOR FILING DATE: 1997-10-10  
PRIOR APPLICATION NUMBER: US 60/145,746  
PRIOR FILING DATE: 1998-03-03  
PRIOR APPLICATION NUMBER: US 09/168,888  
PRIOR FILING DATE: 1998-10-09  
PRIOR APPLICATION NUMBER: US 09/947,387  
PRIOR FILING DATE: 2001-09-07  
NUMBER OF SEQ ID NOS: 142  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 142  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
OTHER INFORMATION: Peptide  
US-10-829-381-142  
Query Match 100.0%; Score 21; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;  
Qy 1 YYAD 4  
Db 1 YYAD 4

RESULT 9  
US-09-394-019B-42  
Sequence 42, Application US/09394019B  
GENERAL INFORMATION:  
APPLICANT: Oncoimmunin, Inc.  
APPLICANT: Konoriva, Akira  
APPLICANT: Packard, Beverly  
TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL SAMPLES AND METHODS OF USE THEREOF  
FILE REFERENCE: 300/903620US  
CURRENT APPLICATION NUMBER: US/09/394,019B  
CURRENT FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: PCT/US98/00300  
PRIOR FILING DATE: 1998-02-20  
NUMBER OF SEQ ID NOS: 405  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO: 42  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic peptide substrate  
FEATURE:

RESULT 10  
 US-09-394-019B-43  
 Query Match Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid

Qy 1 YYAD 4  
 Db 4 YYAD 7

RESULT 11  
 US-09-394-019B-43  
 Query Match Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OTHER INFORMATION: Xaa can be any naturally occurring amino acid

Qy 1 YYAD 4  
 Db 4 YYAD 7

RESULT 12  
 US-09-394-019B-288  
 Query Match Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid

Qy 1 YYAD 4  
 Db 4 YYAD 7

RESULT 13  
 US-09-394-019B-42  
 Query Match Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid

Qy 1 YYAD 4  
 Db 4 YYAD 7

RESULT 14  
 US-09-394-019B-287  
 Query Match Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid

Qy 1 YYAD 4  
 Db 4 YYAD 7

RESULT 15  
 US-09-394-019B-288  
 Query Match Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid

Qy 1 YYAD 4  
 Db 4 YYAD 7

RESULT 16  
 US-09-394-019B-288  
 Query Match Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid

Qy 1 YYAD 4  
 Db 4 YYAD 7

RESULT 17  
 US-09-394-019B-288  
 Query Match Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid

Qy 1 YYAD 4  
 Db 4 YYAD 7

RESULT 18  
 US-09-394-019B-288  
 Query Match Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid

Qy 1 YYAD 4  
 Db 4 YYAD 7

RESULT 19  
 US-09-394-019B-288  
 Query Match Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid

Qy 1 YYAD 4  
 Db 4 YYAD 7

RESULT 20  
 US-09-394-019B-288  
 Query Match Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid

Qy 1 YYAD 4  
 Db 4 YYAD 7

TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
 / FILE REFERENCE: M-903820US  
 / CURRENT FILING DATE: 1999-09-10  
 / PRIOR APPLICATION NUMBER: PCT/US98/00300  
 / PRIOR FILING DATE: 1998-02-20  
 / PRIOR APPLICATION NUMBER: US 08/802,981  
 / NUMBER OF SEQ ID NOS: 257  
 / SOFTWARE: PatentIn version 3.0  
 / SEQ ID NO 42  
 / LENGTH: 14  
 / TYPE: PRT  
 / ORGANISM: Artificial  
 / FEATURE:  
 / OTHER INFORMATION: Synthetic peptide substrate  
 / FEATURE:  
 / NAME/KEY: MOD\_RES  
 / LOCATION: (3) .. (3)  
 / OTHER INFORMATION: Xaa is Aib  
 US-09-394-019B-42

Query Match 100.0%; Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18; Mismatches 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Name/KEY: MOD\_RES  
 Qy 1 YVAD 4  
 Db 4 YVAD 7

RESULT 14  
 US-09-394-019B-43  
 / Sequence 43, Application US/09394019B  
 / GENERAL INFORMATION:  
 / APPLICANT: Oncoimmunin, Inc.  
 / APPLICANT: Komoriya, Akira  
 / APPLICANT: Packard, Beverly  
 / TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
 / FILE REFERENCE: M-903820US  
 / CURRENT FILING DATE: 1999-09-10  
 / PRIOR APPLICATION NUMBER: PCT/US98/00300  
 / PRIOR FILING DATE: 1998-02-20  
 / PRIOR APPLICATION NUMBER: US 08/802,981  
 / NUMBER OF SEQ ID NOS: 257  
 / SOFTWARE: PatentIn version 3.0  
 / SEQ ID NO 43  
 / LENGTH: 14  
 / TYPE: PRT  
 / ORGANISM: Artificial  
 / FEATURE:  
 / OTHER INFORMATION: Synthetic peptide substrate  
 / NAME/KEY: MOD\_RES  
 / LOCATION: (3) .. (3)  
 / OTHER INFORMATION: Xaa is Aib

Sequence 42, Application US/09394019C  
 / GENERAL INFORMATION:  
 / APPLICANT: Oncoimmunin, Inc.  
 / APPLICANT: Komoriya, Akira  
 / APPLICANT: Packard, Beverly  
 / TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
 / FILE REFERENCE: 300-903820US  
 / CURRENT APPLICATION NUMBER: US/09/394,019C  
 / CURRENT FILING DATE: 1999-09-10  
 / PRIOR APPLICATION NUMBER: PCT/US98/00300  
 / PRIOR FILING DATE: 1998-02-20  
 / PRIOR APPLICATION NUMBER: US 08/802,981  
 / NUMBER OF SEQ ID NOS: 405  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO 42  
 / LENGTH: 14  
 / TYPE: PRT  
 / ORGANISM: Artificial  
 / FEATURE:  
 / OTHER INFORMATION: Synthetic peptide substrate  
 / NAME/KEY: MOD\_RES  
 / LOCATION: (3) .. (3)  
 / OTHER INFORMATION: X is Aib  
 / FEATURE:  
 / NAME/KEY: misc feature  
 / LOCATION: (3) .. (3)  
 / OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
 US-09-394-019C-42

Query Match 100.0%; Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18; Mismatches 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 4; Name/KEY: misc feature  
 Qy 1 YVAD 4  
 Db 4 YVAD 7

Search completed: May 24, 2004, 14:48:20  
 Job time : 13.5 secs

Query Match 100.0%; Score 21; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 18; Mismatches 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 4; Name/KEY: misc feature  
 Qy 1 YVAD 4  
 Db 4 YVAD 7

RESULT 15  
 US-09-394-019C-42

GenCore version 5.1.6  
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OM Protein - protein search, using sw mode!  
Run on: May 24, 2004, 14:36:18 ; Search time 13.5 Seconds  
(without alignments)  
28.501 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : PIR 78.4\*

1: pir1 \*  
2: pir2 \*  
3: pir3 \*  
4: pir4 \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	32	S20719	alcohol dehydrogenase related protein (EC 1.1.1.1) - fruit fly (Drosophila yakuba) (fr)
2	21	100.0	43	A24553	N;Alternate names: Adh-dup protein; Adh-related protein; Adhr protein; alcohol dehydrogenase
3	21	100.0	54	H82718	C;Species: Drosophila yakuba
4	21	100.0	66	PC4222	C;Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 11-Jun-1999
5	21	100.0	66	PC4266	R;Accession: S20719
6	21	100.0	68	G82969	R;Ashburner, M.
7	21	100.0	75	A24554	Submitted to the EMBL Data Library, July 1990
8	21	100.0	76	S51629	A;Reference number: S20713
9	21	100.0	77	R3BS18	A;Accession: S20719
10	21	100.0	80	A61613	A;Molecule type: DNA
11	21	100.0	82	I51103	A;Residues: 1-32 <ASH>
12	21	100.0	82	I51106	A;Cross-references: EMBL:X54120; PIDN:99214; PMID:CAA38064.1; PID:99216
13	21	100.0	82	E71321	C;Genetics:
14	21	100.0	86	A28093	A;Gene: FlyBase:Adhr; Adh-dup
15	21	100.0	88	S71291	A;Cross-references: FlyBase:FBgn10013164
16	21	100.0	88	H67560	C;SuperFamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
17	21	100.0	94	G69957	C;Keywords: oxidoreductase
18	21	100.0	94	A62197	
19	21	100.0	95	A49027	
20	21	100.0	97	H42409	
21	21	100.0	97	AD2153	
22	21	100.0	98	F9952	
23	21	100.0	99	A97437	
24	21	100.0	101	A47450	
25	21	100.0	102	T92100	
26	21	100.0	102	B89860	
27	21	100.0	106	D50247	
28	21	100.0	112	C33766	
29	21	100.0	113	D27664	

#### ALIGNMENTS

RESULT 1  
S20719  
alcohol dehydrogenase related protein (EC 1.1.1.1) - fruit fly (Drosophila yakuba) (fr)  
N;Alternate names: Adh-dup protein; Adh-related protein; Adhr protein; alcohol dehydrogenase

C;Species: Drosophila yakuba

C;Date: 20-Feb-1995 #sequence\_revision 19-Apr-1996 #text\_change 11-Jun-1999

R;Accession: S20719

R;Ashburner, M.

Submitted to the EMBL Data Library, July 1990

A;Reference number: S20713

A;Accession: S20719

A;Molecule type: DNA

A;Residues: 1-32 <ASH>

A;Cross-references: EMBL:X54120; PIDN:99214; PMID:CAA38064.1; PID:99216

C;SuperFamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C;Keywords: oxidoreductase

Query Match Score 21; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YYAD 4  
Db 11 YYAD 14

RESULT 2  
A24553  
cuticle protein SC1 - flesh fly (Sarcophaga bullata) (fragment)  
C;Species: Sarcophaga bullata  
C;Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 18-Jun-1993  
R;Accession: A24553  
C;Reference number: A24553  
R;Henzel, W.J.; Mole, J.E.; Mulligan, K.; Lipek, H.  
J. Mol. Evol. 22, 39-45, 1985  
A;Title: Sarcophagid larval proteins: partial sequence homologies among three cuticle  
A;Reference number: A92963; PMID:86037264; PMID:3932663  
A;Accession: A24553  
A;Molecule type: protein  
A;Residues: 1-43 <HEN>  
C;SuperFamily: cuticle protein LCP1  
C;Keywords: 1-43 <HEN>

Query Match Score 21; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YYAD 4  
Db 39 YYAD 42

## RESULT 3

## RESULT 5

HB2718 hypothetical protein XP1129 [Imported] - *Xylella fastidiosa* (strain 9a5c)  
 C;Species: *Xylella fastidiosa*  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C;Accession: HB2718  
 R;Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen  
 Nature 406, 151-157, 2000  
 A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.  
 A;Reference number: A8515; MUID:2036577; PMID:10910347  
 A;Note: for a complete list of authors see reference number A59328 below  
 A;Accession: HB2718  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-54 <SIM>  
 A;Cross references: GB:AE003849; GB:AE003849; NID:9106088; PIDN:AAF83939.1; GSPDB:GN001  
 A;Experimental source: strain 9a5c  
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.A.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;  
 Briones, M.R.P.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, F.  
 as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
 Submitted to Genbank, June 2000  
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, S.C.; Franca, M.C.; Frohn, J.D.; Junqueira, M.L.; Kempter, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.; Laige-Abdalla, M.A.; Maddeira, A.M.B.N.; Madeira, H.M.F.; Marro, C.L.; Marques, M.V.; Martins, E.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
 A;Genetics: Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmeiro, D.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.R.; de Sa, R.G.; Santelli, R.V.; Sawaaski M.; Tsubak, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;  
 A;Reference number: A59328  
 C;Genetics: XF1129

Query Match 100.0%; Score 21; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YYAD 4  
 Db 7 YYAD 10

RESULT 4  
 PC222 GTP-binding protein rhoA - pig (fragment)

C;Species: *Sus scrofa domestica* (domestic pig)  
 C;Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 20-Jun-2000  
 C;Accession: PC4222  
 R;Nishimura, J.; Sakihara, C.; Zhou, Y.; Kanaide, H.  
 Biochem Biophys Res Commun 227, 750-754, 1996  
 A;Title: Expression of rho A and rho kinase mRNAs in porcine vascular smooth muscle.  
 A;Reference number: PC4222; MUID:97040692; PMID:9886005  
 A;Accession: PC4222  
 A;Molecule type: mRNA  
 A;Residues: 1-66 <NIS>  
 A;Cross-references: DDBJ:DR9492; NID:91695730; PIDN:BA13966.1; PID:91695731  
 C;Comment: This protein is involved in the inhibition of myosin light chain phosphatase.  
 C;Genetics:

A;Gene: rhoA  
 C;Superfamily: ras transforming protein; translation elongation factor Tu homology  
 C;Keywords: GTP binding

Query Match 100.0%; Score 21; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4  
 Db 64 YYAD 67

RESULT 4  
 PC222 GTP-binding protein rhoA - rat (fragment)

C;Species: *Rattus norvegicus* (Norway rat)  
 C;Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 13-Aug-1999  
 C;Accession: PC4266  
 R;Nishimura, J.; Sakihara, C.; Nakano, H.; Kanaide, H.  
 Biochem Biophys Res Commun 230, 356-359, 1997  
 A;Title: Up-regulation of rho A and rho-kinase mRNAs in the rat myometrium during pregn  
 A;Reference number: PC4266; MUID:9168976; PMID:9016783  
 A;Accession: PC4266  
 A;Molecule type: mRNA  
 A;Residues: 1-66 <NII>  
 C;Comment: This protein is involved in the Ca2+ sensitivity of the smooth muscle myofil  
 C;Superfamily: ras transforming protein; translation elongation factor Tu homology  
 C;Keywords: GTP binding

Query Match 100.0%; Score 21; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4  
 Db 7 YYAD 10

RESULT 7  
 AC1251 hypothetical protein lmc1411 [Imported] - *Listeria monocytogenes* (strain EGD-e)

C;Species: *Listeria monocytogenes*  
 C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
 C;Accession: AC1251  
 R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blooecke, H.; Dominguez-Bernal, G.; Duchaude, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Science 294, 849-851, 2001  
 A;Authors: Kreit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mo, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland  
 A;Title: Comparative Genomics of *Listeria* species  
 A;Reference number: AB1077; MUID:2153279; PMID:11679659  
 A;Accession: AC1251  
 A;Status: preliminary  
 A;Molecule type: DNA

A;Residues: 1-75 <GLA>  
 A;Cross-references: GB:NC\_003210; PIDN: CAC99489\_1; PID: g16410840; GSPDB:GN00177  
 A;Experimental source: strain EGD-e  
 C;Genetics:  
 A;Gene: lm01411

Query Match Similarity 100.0%; Score 21; DB 2; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YYAD 4  
 Db 65 YYAD 68

RESULT 8  
 S51629 PRFAC-6 Protein - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Accession: S51629  
 C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 24-Sep-1999  
 R;Pierrou, S.; Hellqvist, M.; Samuelsson, L.; Enerbaeck, S.; Carlsson, P.  
 EMBO J. 13, 5002-5012, 1994  
 A;Title: Cloning and characterization of seven human forkhead proteins: binding site specificities, dimerization domains, and expression patterns  
 A;Reference number: S51624; MUID: 9504532; PMID: 7957066  
 A;Accession: S51629  
 A;Status: preliminary; nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-76 <PIE>  
 A;Cross-references: EMBL:U13224; NID: g563167; PIDN: AA92041\_1; PID: 9563168  
 C;Genetics:

A;Gene: GDB:FKHL10; PRFAC6  
 A;Cross-references: GDB:450228; OMIM:601093  
 A;Map position: 5q34-5q34  
 C;Superfamily: unassigned fork head proteins\_fork head DNA-binding domain homology (fragment) <FHD>  
 P;6/76/Domain: fork head DNA-binding domain homology

Query Match Similarity 100.0%; Score 21; DB 2; Length 76;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YYAD 4  
 Db 35 YYAD 38

RESULT 9  
 R3B818 ribosomal protein S18 - *Bacillus stearothermophilus*  
 C;Species: *Bacillus stearothermophilus*  
 C;Accession: S03556  
 R;McDougal, J.; Choli, T.; Kruft, V.; Kapp, U.; Wittmann-Liebold, B.  
 FEBS Lett. 245, 253-260, 1989  
 A;Title: The complete amino acid sequence of ribosomal protein S18 from the moderate thermophile  
 A;Reference number: S03556; MUID: 8917319; PMID: 2647521  
 A;Accession: S03556  
 A;Molecule type: protein  
 A;Residues: 1-77 <MCD>  
 C;Superfamily: *Escherichia coli* ribosomal protein S18  
 C;Keywords: protein biosynthesis; ribosome

Query Match Similarity 100.0%; Score 21; DB 1; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YYAD 4  
 Db 73 YYAD 76

RESULT 10  
 AG1613

Query Match 100.0%; Score 21; DB 2; Length 82;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 42 YVAD 45

RESULT 13

E71321 hypothetical protein TP0467 - syphilis spirochete  
C;Species: Treponema pallium subsp. Pallidum (syphilis spirochete)  
C;Date: 24-Jul-1995 #sequence\_revision 24-Jul-1995 #text\_change 05-Nov-1999  
C;Accession: E71321  
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
rson, J.; Khakak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDaniel  
They, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 37-38, 1998  
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A;Reference number: A71250; MUID:98332770; PMID:9665876  
A;Accession: E71321  
A;Status: preliminary; nucleic acid sequence not shown;  
A;Molecule type: DNA  
A;Residues: 1-82 <COL>  
A;Cross-references: GB:AB001223; GB:AE000520; NID:93322745; PID:ANG65458.1; PMID:9332275  
A;Experimental source: strain Nichols  
C;Genetics:  
A;Gene: TP0467

Query Match 100.0%; Score 21; DB 2; Length 82;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 31 YVAD 34

Qy 1 YVAD 4  
Db 15 YVAD 18

RESULT 15

E71291 retrovirus-related reverse transcriptase homolog (clone Rtat3) - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Strain: Columbia  
A;Variety: strain Columbia  
C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
C;Accession: S71291  
R;Brändes, A.; Heslop-Harrison, J.S.; Kamm, A.; Kubis, S.; Doudrick, R.L.; Schmidt, T.  
submitted to the EMBL Data Library, January 1996  
A;Description: Comparative analysis of the chromosomal and genomic organization of Ty1-  
A;Reference number: S71291  
A;Accession: S71291  
A;Molecule type: DNA  
A;Residues: 1-88 <COL>  
A;Cross-references: EMBL:Z68911; NID:Sl171493; PID:CAA93146.1; PMID:Sl171494

Qy 1 YVAD 4  
Db 20 YVAD 23

RESULT 16

A28033 GTP-binding protein rhoB - bovine (fragments)  
N;Alternate name: 20K GTP-binding protein rho; rhoB\* protein; transforming protein rhoB  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 26-Jan-1989 #sequence\_revision 05-Apr-1995 #text\_change 13-Aug-1999  
C;Accession: A28033; B28324; E60050  
R;Yamamoto, K.; Kondo, J.; Hishida, T.; Teranishi, Y.; Takai, Y.  
J. Biol. Chem. 263, 9926-9932, 1988  
A;Title: Purification and characterization of a GTP-binding protein with a molecular weight  
A;Reference number: A28093; MUID:88251127; PMID:3133371  
A;Accession: A28093  
A;Molecule type: protein  
A;Residues: 1-134-48-53-59-71 <WIL>  
A;Experimental source: brain  
R;Kondo, J.; Kikuchi, A.; Yamamoto, K.; Takai, Y.  
Brain Res. Mol. Brain Res. 7, 9-16, 1990  
A;Title: Purification and characterization of a GTP-binding protein with a molecular weight  
C1;Identification as the rhoA gene product  
A;Reference number: A38324; MUID:91065876; PMID:2174426  
A;Accession: B28324  
A;Molecule type: protein  
A;Residues: 54-68-72-86 <HO2>  
A;Experimental source: brain  
C;Genetics:  
A;Gene: rhoB

C;Superfamily: ras transforming protein; translation elongation factor Tu homology  
C;Keywords: GTP binding immediate-early protein; transforming protein  
F;51-54/Region: GTP-binding NRKD motif

Query Match 100.0%; Score 21; DB 2; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 15 YVAD 18

RESULT 15

S71291 retrovirus-related reverse transcriptase homolog (clone Rtat3) - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Strain: Columbia  
A;Variety: strain Columbia  
C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
C;Accession: S71291  
R;Brändes, A.; Heslop-Harrison, J.S.; Kamm, A.; Kubis, S.; Doudrick, R.L.; Schmidt, T.  
submitted to the EMBL Data Library, January 1996  
A;Description: Comparative analysis of the chromosomal and genomic organization of Ty1-  
A;Reference number: S71291  
A;Accession: S71291  
A;Molecule type: DNA  
A;Residues: 1-88 <COL>  
A;Cross-references: EMBL:Z68911; NID:Sl171493; PID:CAA93146.1; PMID:Sl171494

Qy 1 YVAD 4  
Db 20 YVAD 23

Query Match 100.0%; Score 21; DB 2; Length 88;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 20 YVAD 23

Query Match 100.0%; Score 21; DB 2; Length 88;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 20 YVAD 23

Search completed: May 24, 2004, 14:41:39  
Job time : 14.5 secs

Scoring table:	BLOSUM62	Gapop 10.0 , Gapext: 0.5	Perfect score:	21	Sequence:	1 YVAD 4	Scanned:	141681 seqs, 52070155 residues	Total number of hits satisfying chosen parameters:	141681	Post-processing:	Maximum Match 100% Listing first 45 summaries	Database :	SwissProt_42;*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext: 0.5	Perfect score:	21	Sequence:	1 YVAD 4	Scanned:	141681 seqs, 52070155 residues	Total number of hits satisfying chosen parameters:	141681	Post-processing:	Maximum Match 100% Listing first 45 summaries	Database :	SwissProt_42;*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES
Result No.	Score	Query Match	Length	DB	ID	Description										
1	21	100.0	32	1	ADHR_DROYA	P28487 drosophila										
2	21	100.0	36	1	PAHO_RABBIT	P11336 oryctolagus										
3	21	100.0	37	1	ATPO_DROME	P80504 solenopsa										
4	21	100.0	43	1	CTDP1_SARBU	P14485 sarcophaga										
5	21	100.0	74	1	RS18_CHLTER	Q8ram3 chloroforid										
6	21	100.0	75	1	HE15_RHOFRB	P80382 rhoofexa										
7	21	100.0	77	1	RS18_BACST	P10306 bacillus st										
8	21	100.0	82	1	Y467_TREPA	P8480 treponema p										
9	21	100.0	94	1	YQCV_BACSU	P51499 bacillus su										
10	21	100.0	102	1	CPA1_CANPG	P81175 cancer pagu										
11	21	100.0	104	1	LCPS5_DROME	P92192 drosophila										
12	21	100.0	105	1	CPA2_CANPG	P81576 cancer pagu										
13	21	100.0	113	1	Y930_MYCTU	Q10168 mycobacteri										
14	21	100.0	117	1	GHHA_ACALA	P30370 acanthopae										
15	21	100.0	122	1	TVB5_MOUSE	P02123 mus musculu										
16	21	100.0	125	1	CU14_MANSE	P13229 manduca sexta										
17	21	100.0	126	1	CLP2_DROME	P91129 drosophila										
18	21	100.0	138	1	CP11_DROMI	P91627 drosophila										
19	21	100.0	143	1	CU17_BOMMO	Q94519 drosophila										
20	21	100.0	152	1	ACPM_DROME	P80518 araneus dia										
21	21	100.0	156	1	CT05_ARADI	P80519 araneus dia										
22	21	100.0	159	1	CU57_ARADI	P07435 bos taurus										
23	21	100.0	159	1	OBP_BOVIN	P24431 zea mays										
24	21	100.0	161	1	HE21_MAIZE	Q915t7 neisseria m										
25	21	100.0	163	1	DD2_NEIMA	Q10301 orgyia pseu										
26	21	100.0	171	1	Y041_NEVOP	Q99t6v staphylococ										
27	21	100.0	174	1	ATROK_STPAM	Q8BWC8 bombyx mori										
28	21	100.0	174	1	CT02_BOMMO	P02388 bombyx mori										
29	21	100.0	174	1	CTSH_RHITR	Q83379 rhizobium t										
30	21	100.0	180	1	APT_PSPK	Q8B333 pseudomonas										
31	21	100.0	182	1	ND0C_RHILT	P04t78 rhizobium l										
32	21	100.0	182	1	CUPP_DROME	P14t84 drosophila										
33	21	100.0	184	1												

## ALIGNMENTS

RESULT 1														
ADHR_DROYA	ID	ADHR_DROYA	STANDARD;	PRT;	32 AA.									
	AC	P28487;												
	DT	01-DEC-1992	(Rel. 24, Created)											
	DT	01-DEC-1992	(Rel. 24, Last sequence update)											
	DT	01-OCT-1996	(Rel. 34, Last annotation update)											
	DE	Alcohol dehydrogenase related 31 kDa protein (Fragment).												
	GN													
	OS	Drosophila yakuba (Fruit fly).												
	OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephdroidea; Drosophilidae; Drosophila; Drosophila.												
	NCBI_TaxID	7245;												
	RN	[1]												
	RP	SEQUENCE FROM N.A.												
	RA	Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.												
	CC	-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.												
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	CC	(SDR) family.												
	CC	DR	PIR: S20719; S20719.											
	DR	Protein; PBrn012364; Dyak; Adhr.												
	DR	InterPro; IPR02198; Adh_short.												
	DR	PROSITE; PS00061; Adh_short; PARTIAL.												
	KW	Oxidoreductase.												
	PT	NP_BIND	11											
	FT	NON_TER	32											
	SQ	SEQUENCE	32 AA;	3412 MW;	9302949AFCBED4F CRC64;									
	Query	Query Match				Score 21;	Length 32;							
						Pred. No. 28;								
						Best Local Similarity 100.0%;								
						Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
						Qy	1 YVAD 4							
						Db	11 YVAD 14							

## RESULT 2

## PAHO\_RABBIT

## STANDARD;

## PRT;

## 36 AA.

## AC

## P41376;

## DT

## 01-FEB-1995 (Rel. 31, Created)

## DT

## 01-FEB-1995 (Rel. 31, Last sequence update)

## DT

## 10-OCT-2003 (Rel. 42, Last annotation update)

## DT

## Pancreatic hormone (Pancreatic polypeptide) (PP).

## DB



RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D., Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.; "The complete genome sequence of Chlorobacter tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium"; Proc. Natl. Acad. Sci. U.S.A. 99:9509-9511 (2002).

CC -!- FUNCTION: Binds as a heterodimer with protein S6 to the central domain of the 16S rRNA, where it helps stabilize the platform of the 30S subunit (By similarity).

CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight heterodimer with protein S6 (By similarity).

CC -!- SIMILARITY: Belongs to the S18P family of ribosomal proteins.

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CC EMBL: AE012662; AAC73349.1; - .

DR TIGR; CT2133; .

DR HAMAP; MF\_00270; / .

DR InterPro; IPR001648; Ribosomal\_S18; .

DR Pfam; PF01084; Ribosomal\_S18; T.

DR PRINTS; PRO00974; RIBOSOMAL\_S18; .

DR PRODOM; PD002239; Ribosomal\_S18; 1.

DR TIGRFAMS; TIGR00165; S18; 1.

DR PROSITE; PS00057; RIBOSOMAL\_S18; FALSE\_NEG.

DR RIBOSOMAL Protein; RNA-binding; rRNA-b-binding; Complete proteome.

KW SEQUENCE 74 AA; 8671 MW; 7120CA25284DB8B CRC64;

CC Query Match 100.0%; Score 21; DB 1; Length 74; Best Local Similarity 100.0%; Pred. No. 65; Gaps 0; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 YYAD 4

CC Db 68 YYAD 71

RESULT 6

HP-1S\_RHOFE ID HPS\_RHOFE STANDARD; PRT; 75 AA.

AC P0882; MEDLINE=97334565; PubMed=9119002;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE High potential iron-sulfur protein (HiPIP).

GN HiPIP.

CC Rhodofrax fermentans.

CC Proteobacteria; Betaproteobacteria; Burkholderiales;

CC Comamonadaceae; Rhodobacter.

CC [1] NCBI\_TaxID=280666;

RN RP SEQUENCE.

CC RX MEDLINE=97334565; PubMed=9119002;

CC RA van Driesche G., Ciurli S., Hochkoeppler A., van Beumen J.J.;

CC RT "The primary structure of Rhodofrax fermentans high-potential iron-sulfur protein, an electron donor to the photosynthetic reaction center"; Eur. J. Biochem. 244:371-377 (1997).

CC -!- FUNCTION: Specific class of high-redox-potential 4Fe-4S ferredoxins. Functions in anaerobic electron transport in most purple and in some other photosynthetic bacteria and in at least one genus (Paracoccus) of halophilic, denitrifying bacteria.

CC -!- SUBUNIT: Hemodimer (By similarity).

CC -!- SIMILARITY: Belongs to the high potential iron-sulfur protein (HiPIP) family.

CC HSSP; P00266; 1CKU.

DR InterPro; IPR000170; Hipot\_ironsulf.

DR Pfam; PF01355; H1PIP; 1.

DR PROSITE; PS00596; H1PIP; 1.

KW "The complete genome sequence of Chlorobacter tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium"; Proc. Natl. Acad. Sci. U.S.A. 99:9509-9511 (2002).

CC -!- FUNCTION: Binds as a heterodimer with protein S6 to the central domain of the 16S rRNA, where it helps stabilize the platform of the 30S subunit (By similarity).

CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight heterodimer with protein S6 (By similarity).

CC -!- SIMILARITY: Belongs to the S18P family of ribosomal proteins.

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CC EMBL: AE012662; AAC73349.1; - .

DR TIGR; CT2133; .

DR HAMAP; MF\_00270; / .

DR InterPro; IPR001648; Ribosomal\_S18; .

DR Pfam; PF01084; Ribosomal\_S18; T.

DR PRINTS; PRO00974; RIBOSOMAL\_S18; .

DR PRODOM; PD002239; Ribosomal\_S18; 1.

DR TIGRFAMS; TIGR00165; S18; 1.

DR PROSITE; PS00057; RIBOSOMAL\_S18; FALSE\_NEG.

DR RIBOSOMAL Protein; RNA-binding; rRNA-b-binding; Complete proteome.

KW SEQUENCE 74 AA; 8671 MW; 7120CA25284DB8B CRC64;

CC Query Match 100.0%; Score 21; DB 1; Length 75; Best Local Similarity 100.0%; Pred. No. 66; Gaps 0; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 YYAD 4

CC Db 17 YYAD 20

RESULT 7

RS18\_BACST ID RS18\_BACST STANDARD; PRT; 77 AA.

DR P10816; P10816; / .

AC P10816; / .

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB 30S ribosomal protein S18 (BS18) (BS18).

GN RPSR.

OS Bacillus stearothermophilus

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus

OC NCBI\_TaxID=1422;

RN [1] NCBI\_TaxID=1422;

RN [2] PDB\_253\_260(1989).

RP SEQUENCE.

RC STRAIN=799; MEDLINE=83171319; PubMed=2647521;

RC McDougall J., Choi I.T., Krut V., Kapp U., Wittmann-Liebold B.; "The complete amino acid sequence of ribosomal Protein S18 from the moderate thermophile Bacillus stearothermophilus"; FEBS Lett. 249:253-260(1989).

RC SEQUENCE OF 1-15.

RC STRAIN=10; MEDLINE=75019590; PubMed=4607606;

RC Yaguchi M., Matheson A.T., Visentini L.P.; "Prokaryotic ribosomal proteins: N-terminal sequence homologies and structural correspondence of 30 S ribosomal proteins from Escherichia coli and Bacillus stearothermophilus"; FEBS Lett. 46:1296-300(1974).

CC -!- FUNCTION: Binds as a heterodimer with protein S6 to the central domain of the 16S rRNA, where it helps stabilize the platform of the 30S subunit (By similarity).

CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight heterodimer with protein S6 (By similarity).

CC -!- SIMILARITY: Belongs to the S18P family of ribosomal proteins.

DR PIR; S03556; R3BS18.

DR HAMAP; MF\_00270; / .

DR InterPro; IPR001648; Ribosomal\_S18.

DR Pfam; PF01084; Ribosomal\_S18; 1.

DR PRINTS; PRO00974; RIBOSOMAL\_S18; .

DR PRODOM; PD002239; Ribosomal\_S18; .

DR TIGRFAMS; TIGR00165; S18; 1.

DR PROSITE; PS00057; RIBOSOMAL\_S18; 1.

DR RIBOSOMAL Protein; RNA-binding; rRNA-binding.

PT INIT\_MET 0

SQ SEQUENCE 77 AA; 8837 MW; A3F635FC64210E42 CRC64;

CC Query Match 100.0%; Score 21; DB 1; Length 77;

CC Best Local Similarity 100.0%; Pred. No. 68; Gaps 0; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 YYAD 4

CC Db 73 YYAD 76

RESULT 8

Y467\_TREPA STANDARD; PRT; 82 AA.

AC OS3480; PIR: E71321; E71321.

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

ID Hypothetical protein TP0467.

GN TP0467.

OS Treponema pallidum.

Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.

OX NCBI TaxID=160;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=Nichols;

RX MEDLINE=9665876; PubMed=9665876;

RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G., Dodson R., Gwynn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.,

RT "Complete genome sequence of *Treponema pallidum*, the syphilis spirochete." Science 281:375-388 (1998).

RL

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CC EMBL; AB001223; AAC65458..1; -.

DR PIR: TP0467;

DR HYPOTHETICAL PROTEIN; Complete proteome;

SQ SEQUENCE 82 AA; 9614 MW; PDBA60CBE370890C CRC64;

Query Match 100.0%; Score 21; DB 1; Length 92;

Best Local Similarity 100.0%; Fred. No. 72;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR YVAD 4

Db 31 YVAD 34

RESULT 9

YQGV\_BACSU STANDARD; PRT; 94 AA.

AC P54459; PIR: E71321; E71321.

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

KW Hypothetical protein yqgv.

GN YQGV OR ESG24810.

OS *Bacillus subtilis*.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

OX NCBI TaxID=1423;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=16B / JH642;

RX MEDLINE=97124195; PubMed=8969508;

RA Mizuno M., Masuda S., Takemaru R.-I., Hosono S., Sato T., Takeuchi M., Kobayashi Y.

RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of the *Bacillus subtilis* genome containing the *skin* element and many sporulation genes.";

RL Microbiology 142:3103-3111 (1996).

RN [2]

SEQUENCE FROM N.A.

RP STRAIN=16B;

RC MEDLINE=98044033; PubMed=9384377;

RX KUNST F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Bologin A., Borchert S., Brune M., Brignell S.C., Bron S., Borriss R., Bourterre L., Brans A., Braun M., Capano L., Carter N.M., Choi S.K., Codani J.J., Conner I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmeron P.T., Entian K.D., Errington J., Fabre C., Ferrari E., Fouger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly B.J., Grandi G., Guiseppi G., Guy B.J., Hailej J., Harwood C.R., Henaut A., Hilpert H., Hollaspeel S., Hosono S., Hullio M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaeber-Blanchard M., Klein C., Kubiyashi Y., Koetter P., Koningsstein P., Krogh S., Kunano M., Lapidot A., Lardinois S., Laiher J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medina R., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portebeau D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Rocic M., Sadie Y., Sato T., Scanlan E., Schleicher S., Schroeter R., Soffone F., Soldo B., Sorokin A., Taccioni B., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandembol M., Vanner F., Vassarotti A., Vizari A., Wambutt R., Wedler B., Wedler H., Weitzneger T., Winters P., Wipat A., Yamamoto H., Yamamoto K., Yata K., Yoshida K., Yoshihara H., Zumstein E., Yoshikawa H., Danchin A.; subtilis;

RT Nature 390:249-256 (1997).

CC -!- SIMILARITY: BELONGS TO THE UPF0045 FAMILY.

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CC -!- SIMILARITY: BELONGS TO THE UPF0045 FAMILY.

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CC EMBL; D84432; BAA1525..1; -.

DR EMBL; 299116; CAB1412..1; -.

DR PIR; G69957; G69957.

DR Sublist: BG11689; yqgv.

DR InterPro; IPR002767; DUF77.

DR PFam; PF01310; DUFT77; 1.

DR TIGRFAMS; TIGR00106; TIGR00106; 1.

KW Hypothetical protein; Complete proteome

SEQUENCE 94 AA; 10453 MW; 4A576F233B80999 CRC64;

QY 1 YVAD 4

Db 21 YVAD 24

RESULT 10

CP01\_CAMPG STANDARD; PRT; 102 AA.

AC P81575; P81575;

DR 15-DEC-1998 (Rel. 37, Created)

DR 15-DEC-1998 (Rel. 37, Last sequence update)

DR 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cuticle protein AM/CP0114 (CPAM/CPAM114).

OS Cancer pagurus (Rock crab).  
 OC Bivalvia; Metazoa; Crustacea; Malacostraca;  
 OC Eumalacostraca; Decapoda; Pleocyemata; Brachyura;  
 OC Subbrachyura; Cancroidea; Cancridae; Cancer.  
 OX NCBI\_TAXID=6755;  
 [1] RN  
 RP  
 RC TISSUE-Carapace cuticle;  
 RX MEDLINE=93054472; PubMed=10425740;  
 RA  
 RA  
 RT "Exoskeletal proteins from the crab, *Cancer pagurus*.";  
 RL Comp. Biochem. Physiol. 123A:203-211 (1999).  
 CC -1- TISSUE\_SPECTROSCOPY: Articular membrane and calcified shell.  
 CC -1- MASS\_SPECTROMETRY: MW=11139.8; METHOD=VALDI.  
 CC -1- SIMILARITY: Contains 1 cuticle consensus domain.  
 DR InterPro-IPR000619: Insect cuticle.  
 DR Pfam: PF00319; Chitinbind\_4\_1.  
 DR PRINTS: PRO00231; CUTICLE; FALSE\_NEG.  
 DR Structural Protein; Cuticle.  
 RW SEQUENCE 102 AA; 11142 MW;  
 SQ 100.0%; Score 21; DB 1; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 90;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4  
 Db 63 YYAD 66

RESULT 11  
 LCPS\_DROME  
 ID LCPS\_DROME STANDARD;  
 AC P92132; O969305;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DB Larval cuticle protein V precursor.  
 GN (LCP65AB1 OR LCP5 OR DCP3 ALPHA OR CG18776) AND  
 GN (LCP65AB2 OR LCP5 OR DCP3-BETA OR CG18773).  
 OS Drosophila melanogaster (Pruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Ephemeroidea; Drosophilidae; Drosophila.  
 NCBI\_TAXID=2727;  
 [1] RN  
 RP  
 RC STRAIN=Oregon-R;  
 RA Mandalaparty P.; Jiang S.; Schneider G.; Chihara C.;  
 RT "The cuticle proteins of *Drosophila melanogaster*: sequence of Lcps in  
 the third chromosome cluster.";  
 RL Dros. Info. Service 77:49-51 (1996).  
 RN  
 RP  
 RC STRAIN=Oregon-R;  
 RA MEDLINE=98013412; PubMed=938304;  
 RT Charles J.-P.; Chihara C.; Nejed S.; Riddiford L.M.;  
 RT "A cluster of cuticle genes of *Drosophila* at 65A: sequence, structure  
 and evolution.";  
 RT Genetics 147:1213-1224 (1997).  
 [3] RN  
 RP  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D.; Celniker S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.;  
 RA Amanatides P.G.; Scherer S.E.; Li P.W.; Hoskins R.A.; Gallo R.F.;  
 RA George R.A.; Lewis S.E.; Richards S.; Ashburner M.; Henderson S.N.;  
 RA Sutton G.G.; Worman J.R.; Yandell M.D.; Zhang Q.; Chen L.X.;  
 RA Brandon R.C.; Rogers Y.-H.C.; Blazzz R.G.; Chmpse M.; Pfeiffer B.D.;  
 RA Wan K.H.; Doyle C.; Baxter B.G.; Heit G.; Nelson C.R.; Miklos G.L.G.;  
 RA Abril J.F.; Agbayani A.; An H.-J.; Andrews-Pfannkoch C.; Baldwin D.;  
 RA Ballew R.M.; Basu A.; Baxendale J.; Bayraktaroglu L.; Beasley E.M.;

RESULT 12  
 LCPS\_DROME  
 ID LCPS\_DROME STANDARD;  
 AC P92132; O969305;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DB Larval cuticle protein V precursor.  
 GN (LCP65AB1 OR LCP5 OR DCP3 ALPHA OR CG18776) AND  
 GN (LCP65AB2 OR LCP5 OR DCP3-BETA OR CG18773).  
 OS Drosophila melanogaster (Pruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Ephemeroidea; Drosophilidae; Drosophila.  
 NCBI\_TAXID=2727;  
 [1] RN  
 RP  
 RC STRAIN=Oregon-R;  
 RA Mandalaparty P.; Jiang S.; Schneider G.; Chihara C.;  
 RT "The cuticle proteins of *Drosophila melanogaster*: sequence of Lcps in  
 the third chromosome cluster.";  
 RL Dros. Info. Service 77:49-51 (1996).  
 RN  
 RP  
 RC STRAIN=Berkeley;  
 RX MEDLINE=98013412; PubMed=938304;  
 RA Charles J.-P.; Chihara C.; Nejed S.; Riddiford L.M.;  
 RT "A cluster of cuticle genes of *Drosophila* at 65A: sequence, structure  
 and evolution.";  
 RT Genetics 147:1213-1224 (1997).  
 [3] RN  
 RP  
 RC STRAIN=Berkeley;

CONFLICT 62 72 AAVHGSPTWV -> CCRPRPHLG (IN REF. 1).  
 SEQUENCE 104 AA; 11267 MW; BA60DD9483DD6992 CRC44;  
 Query Match 100.0%; Score 21; DB 1; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 SY 1 YVAD 4  
 b 84 YVAD 87

RESULT 12  
 CPA2\_CANPG STANDARD; PRT; 105 AA.  
 D CPA2\_CANPG STANDARD; PRT; 105 AA.  
 C P815176;  
 C 15-DEC-1998 (Rel. 37, Created)  
 C 15-DEC-1998 (Rel. 37, Last sequence update)  
 C 28-FEB-2003 (Rel. 41, Last annotation update)  
 C Cuticle protein AM1159 (CPAM1159).  
 C Cancer pagurus (Rock crab).  
 C Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 C Bivalacustraca; Eucarida; Decapoda; Pioecymata; Brachyura;  
 C Brachyura; Cancroidea; Canceridae; Cancer.  
 C NCBI\_TaxID=6755;  
 C [1]  
 C  
 C SEQUENCE.  
 C TISSUE=Carapace cuticle;  
 C MEDLINE=93354412; PubMed=10425740;  
 C Andersen S.O.;  
 C Andersen S.O.;  
 C "Exoskeletal proteins from the crab, Cancer pagurus.";  
 C Comp. Biochem. Physiol. 123A:203-211 (1999).  
 C 1- TISSUE SPECIFICITY: Arthropodial membrane.  
 C 1- MASS SPECTROMETRY: MW=11582.8; METHOD=VALDI.  
 C 1- SIMILARITY: Contains 1 cuticle consensus domain.  
 C Inter-Pro: IPR000618; Insect cuticle.  
 C Pfam: PF00379; Chitin\_bind\_4; 1.  
 C PRINTS: PR00947; CUTICLE.  
 C PROSITE: PS00233; CUTICLE; 1.  
 C STRUCTURAL PROTEIN; CUTICLE.  
 C SEQUENCE 105 AA; 11586 MW; 6C8827FA4E149729 CRC64;  
 C  
 C Query Match 100.0%; Score 21; DB 1; Length 105;  
 C Best Local Similarity 100.0%; Pred. No. 93;  
 C Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 SY 1 YVAD 4  
 b 63 YVAD 66

RESULT 13  
 MTCU9\_0\_MTCU STANDARD; PRT; 113 AA.  
 D MTCU9\_0\_MTCU STANDARD; PRT; 113 AA.  
 C 0108568;  
 C 01-OCT-1996 (Rel. 34, Created)  
 C 01-OCT-1996 (Rel. 34, Last sequence update)  
 C 10-OCT-2003 (Rel. 42, Last annotation update)  
 C Hypothetical protein Rv1990c/Mtb2014/Mb2012c precursor.  
 C RV1990c OR MT2014 OR MTCU39\_29 OR MB2012C.  
 C Mycobacterium tuberculosis, and  
 C Mycobacterium bovis.  
 C Bacteria; Actinobacteria; Actinomycetales;  
 C Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 C NCBI\_TaxID=1773, 1765;  
 C  
 C SEQUENCE FROM N.A.  
 C SPECIES=M tuberculosis; STRAIN=H37-RV;  
 C MEDLINE=98829587; PubMed=9634230;  
 C Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 C Gordon S.V., Brodin P., Garnier T., Barry S., Barry C.E., III, Tekla F.,  
 C Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 C Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 C  
 C

NCBI\_TaxID=8177;

OX [1] SEQUENCE FROM N.A.

RP Tsai H.J.; Chen Y.L.;

RA Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.

RL !- SUBUNIT: Heterodimer of an alpha and a beta chain.

CC !- SUBCELLULAR LOCATION: Secreted.

CC !- SIMILARITY: Belongs to the glycoprotein hormones alpha chain family.

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CC EMBL: M9438; AAA48513; 1; -.

CC HSSP: P01215; 1XUL.

CC InterPro: IPR00200; GF\_cysknot.

CC InterPro: IPR00476; Glyco\_hormone.

CC Pfam: PF00236; hormone6; 1.

CC PRINTS: PR00438; GPROSKNOT.

CC PRODOM: PRO02047; GLYCOPHORMONE; 1.

CC SMART: SM00067; GHA\_1.

CC PROSITE: PS00719; GLICO\_HORMONE\_ALPHA\_1; 1.

CC PROSITE: PS00780; GLICO\_HORMONE\_ALPHA\_2; 1.

CC PROSITE: PS50277; GLICO\_HORMONE\_ALPHA\_3; 1.

CC KW Hormone; Glycoprotein; Signal.

FT SIGNAL 1 23 BY SIMILARITY.

FT CHAIN 24 117 GLYCOPROTEIN HORMONES ALPHA CHAIN.

FT DISULFID 34 57 BY SIMILARITY.

FT DISULFID 37 86 BY SIMILARITY.

FT DISULFID 54 107 BY SIMILARITY.

FT DISULFID 58 109 BY SIMILARITY.

FT DISULFID 65 112 BY SIMILARITY.

FT CARBOXYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOXYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE 117 AA; 13061 MW; P9ACE213DB67AF14 CRC4;

Query Match 100.0% Score 21; DB 1; Length 117;

Best Local Similarity 100.0% Pred. No. 1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4

Db 58 YVAD 61

---

RESULT 15

TVB5\_MOUSE STANDARD; PRT; 122 AA.

ID TVB5\_MOUSE

AC P04213;

DT 20-MAR-1987 (Rel. 04, Created)

DT 20-MAR-1987 (Rel. 04, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB T-cell receptor beta chain V region C5 precursor (Fragment).

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

BN [1]

SEQUENCE FROM N.A.

RX MEDLINE=8503663; PubMed=60929364;

RA Patten P.; Yokota T.; Rothbard J.; Chien Y.; Arai K.; Davis M.M.;

RT "Structure, expression and divergence of T-cell receptor beta-chain variable regions.";

RT Nature 312:40-46 (1994).

CC !- MISCELLANEOUS: This sequence was derived from a T-helper clone.

DR A02008; RWN5C5.

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 36.5 Seconds  
(without alignments)  
34.577 Million cell updates/sec

Title: US-09-765-105a-1

Perfect score: 21

Sequence: 1 YFAD 4

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBM25:\*

1: sp\_archea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mic:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rabbit:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriopl:

17: sp\_archeap:\*

17 100.0 Q8SP33 eudryptula m  
18 100.0 Q8SP34 eudryptula m  
19 100.0 Q8SP51 pygoscelis  
20 100.0 Q8SP40 pygoscelis  
21 100.0 Q8SP37 pygoscelis  
22 100.0 Q8SP43 pygoscelis  
23 100.0 Q8SP38 pygoscelis  
24 100.0 Q8SP32 eudryptula m  
25 100.0 Q8SP31 eudryptula m  
26 100.0 Q8SP35 pygoscelis  
27 100.0 Q8SP42 pygoscelis  
28 100.0 Q8SP44 pygoscelis  
29 100.0 Q8SP45 pygoscelis  
30 100.0 Q8SP41 pygoscelis  
31 100.0 Q8SP39 pygoscelis  
32 100.0 Q8SP31 pseudomonas  
33 100.0 Q8SP47 lactobacillus  
34 100.0 Q8SP48 pygoscelis  
35 100.0 Q8SP40 bifidobacter  
36 100.0 Q93RA0 hydrogenoba  
37 100.0 Q9FP28 listeria mo  
38 100.0 Q8Y784  
39 100.0 Q8AKV5  
40 100.0 Q9TPP9 Gallus galli  
41 100.0 Q9TPP8 Gallus galli  
42 100.0 Q8VMK4 pseudomonas  
43 100.0 Q8BIL9  
44 100.0 Q9WISO human immun  
45 100.0 Q95SE6 human immun

#### ALIGNMENTS

RESULT 1  
ID Q868A6 PRELIMINARY; PRT;  
ID Q868A6 PRELIMINARY; PRT;  
AC Q868A6; PRELIMINARY; PRT;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DB Alcohol dehydrogenase related protein (Fragment).  
GN ADHR.  
OS Drosophila miranda (Pruit fly).  
OC Bokaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydriodea; Drosophilidae; Drosophila;  
NCBI TaxID:7229;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01.01.3, 0101.4, 0101.5, 0101.7, 0101.9, MA32, MA28, SP138,  
RC SP235, SP935, MSH22, and MS138;  
RC Yi S., Bachtrug D., Charlesworth B.;  
RT "A survey of chromosomal and nucleotide sequence variation in  
RT Drosophila miranda";  
RL Genetics 0-0-0(2003);  
DR EMBL; AY338770; AA084926.1;  
DR EMBL; AY238771; AA084920.1;  
DR EMBL; AY238772; AA084923.1;  
DR EMBL; AY338773; AA084932.1;  
DR EMBL; AY238774; AA084934.1;  
DR EMBL; AY238775; AA084936.1;  
DR EMBL; AY238776; AA084938.1;  
DR EMBL; AY238777; AA084940.1;  
DR EMBL; AY238778; AA084942.1;  
DR EMBL; AY238779; AA084944.1;  
DR EMBL; AY238780; AA084946.1;  
DR EMBL; AY238781; AA084948.1;  
FT NON\_TER 32 AA; 3446 MW;  
SQ SEQUENCE 32 AA; 0F0D949AFCB63BE CRC64;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	21	100.0	32	5	Q868A6	drosophila	Q868A6 drosophila
2	21	100.0	44	11	Q8B5J4	Q8B5J4 mus musculus	
3	21	100.0	45	9	Q858A7	Q858A7 mycobacteri	
4	21	100.0	51	7	Q7IP64	Q7IP64 aethia cr-8	
5	21	100.0	52	7	Q11335	Q11335 alligator m	
6	21	100.0	52	7	Q31337	Q31337 alligator m	
7	21	100.0	53	7	Q8ANE1	Q8ANE1 gallinago m	
8	21	100.0	54	16	QPE99	QPE99 xylella fast	
9	21	100.0	62	16	QCY145	QCY145 ralstonia s	
10	21	100.0	62	16	QBXSA4	QBXSA4 ralstonia s	
11	21	100.0	65	16	Q9DP2	Q9DP2 bradyrhizob	
12	21	100.0	66	2	Q9rX3	Q9rX3 streptococc	
13	21	100.0	66	6	P79275	P79275 sub scrofa	
14	21	100.0	66	7	Q8SP36	Q8SP36 pygoscelis	
15	21	100.0	66	7	Q8SP52	Q8SP52 pygoscelis	
16	21	100.0	66	7	Q8SP50	Q8SP50 pygoscelis	



PT	NON_TER	52	52	MW;	D5405D4025C11698	CRC64;
SQ	SEQUENCE	52 AA;	6198	MW;	D5405D4025C11698	CRC64;
Query Match	Best Local Similarity	100.0%;	Score 21;	DB 7;	Length 52;	
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	1	YYAD 4				
Db	24	YYAD 27				
RESULT 6						
Q31337	PRELIMINARY;	PRT;	52 AA.			
ID	Q31337;					
DT	01-NOV-1996 (TRIMBLrel. 01, Created)					
DT	01-JUN-2003 (TRIMBLrel. 24, Last annotation update)					
DS	MHC CLASS II B.					
GN	MHC CLASS II B.					
OS	Alligator mississippiensis (American alligator).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Crocodylia; Aves; Alligatorinae; Alligator.					
OX	NCBI_TaxID:8496;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=American alligator; TISSUE=Blood;					
RX	MEDLINE=96137171; PubMed=8564010;					
RA	Edwards S.V., Grahn M., Potts W.K.					
RT	"Dynamics of Mhc evolution in birds and crocodilians: amplification of class II genes with degenerate primers."					
RT	Mol. Ecol. 4: 719-729 (1995).					
RL	ZMBL;					
DR	GO: GO-0016021; C:integral to membrane; IEA.					
DR	GO: GO-0041012; F:MHC Class II receptor activity; IEA.					
DR	GO: GO-0019884; P:antigen presentation, exogenous antigen; IEA.					
DR	GO: GO-0019886; P:antigen processing, exogenous antigen; IEA.					
DR	InterPro; IPR000353; MHC II_beta.					
DR	Pram; PF00969; MHC II_beta; 1.					
DR	ProDom; PDD00328; MHC II_beta; 1.					
KW	Glycoprotein; MHC II; Transmembrane.					
FT	NON_TER	1	1			
FT	NON_TER	52	52			
SQ	SEQUENCE	52 AA;	6199	MW;	DB4EBDA025C11698	CRC64;
Query Match	Best Local Similarity	100.0%;	Score 21;	DB 7;	Length 52;	
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	1	YYAD 4				
Db	24	YYAD 27				
RESULT 7						
Q38NE1	PRELIMINARY;	PRT;	53 AA.			
ID	Q38NE1;					
AC	Q38NE1;					
DT	01-JUN-2002 (TRIMBLrel. 21, Created)					
DT	01-JUN-2003 (TRIMBLrel. 24, Last annotation update)					
DE	MHC CLASS II antigen B (fragment).					
OS	Gallinago media (Great snipe).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Charadriiformes; Colopacidae; Gallinago; Aves; Neognathae; Charadriiformes; Colopacidae.					
OX	NCBI_TaxID:114734;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Game 6;					
RA	Erblom R., Grahn M., Hoglund J.;					

RT "Patterns of polymorphism in the MHC class II of a non-passerine bird, the Great snipe (Gallinago media).";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR GO: GO-0016021; C:integral to membrane; IEA.  
 DR GO: GO-0045012; F:MHC class II receptor activity; IEA.  
 DR GO: GO-0019884; P:antigen presentation, exogenous antigen; IEA.  
 DR GO: GO-0006955; P:immune response; IEA.  
 DR InterPro; IPR000353; MHC II\_beta.  
 DR Pfam; PF00969; MHC II\_beta; 1.  
 DR Problem; PDD00328; MHC II\_beta; 1.  
 KW Glycoprotein; MHC II; Transmembrane.  
 FT NON\_TER

1	1	1
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FT NON\_TER

53	53	53
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SQ SEQUENCE

53 AA;	6235 MW;	P8A0B0EE3C316727 CRC64;
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Query Match

Best Local Similarity	100.0%;	Score 21;	DB 7;	Length 53;
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Matches 4;

Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Qy

1	YYAD 4
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Db

26	YYAD 29
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RESULT 8

Q9PE99 PRELIMINARY; PRT; 54 AA.

ID Q9PE99 PRELIMINARY; PRT; 54 AA.

AC Q9PE99; PRELIMINARY; PRT; 54 AA.

DT 01-OCT-2000 (TRIMBLrel. 15, Created)

DT 01-OCT-2000 (TRIMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TRIMBLrel. 24, Last annotation update)

DS Hypothetical protein Xf1129.

GN Xf1129.

RA Xylella fastidiosa.

RA Bacteria; Protoplasts; Gammaproteobacteria; Xanthomonadaceae; Xanthomonadaceae; Xylella.

OC

OX NCBI\_TaxID=2371;

RN [1] -

RP SEQUENCE FROM N.A.

RC STRAIN=945C;

RX MEDLINE=20365717; PubMed=10910347;

RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alveranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonacorsini E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carrasco D.M., Carrer H., Coutinho L.L., Cristofolini M., Costa M.C.R., Costa-Neto E., Dia's-Neto E., Docena C., El-Dorry H., El-Dorry H., RN [1] -

RA Garnier M., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Krieger J.E., Kuramae B.E., Laigret F., Lamas M.R., Leite L.C.R., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Machado J.A., Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matosino C.L., Marques M.V., Martins E.A.L., Martins E.M.F., Menck C.P.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nhami A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., Oliveira M.C., Oliveira M.C., Palmeri D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pescquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.C.R., da Silva M., da Silva W.A. Jr., de Souza A.A., da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zattz M., Meidanis J., Setubal J.C., "The genome sequence of the plant pathogen *Xylella fastidiosa*," PIR; AE003949; AF83939.1; -.

DR EMBL; AE003949; AF83939.1; -.

DR PIR; H82718; H82718.

KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 54 AA; 5864 MW; FB7B7C4B250C4B7 CRC64;  
 Query Match 100.0%; Score 21; DB 16; Length 54;  
 Best Local Similarity 100.0%; Fred. No. 3.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YVAD 4  
 Db 50 YVAD 53

RESULT 9  
 Q8Y145 PRELIMINARY; PRT; 62 AA.  
 ID Q8Y145;  
 AC Q8Y145;  
 DT 01-MAR-2002 (TREMBLref. 20, Created)  
 DT 01-MAR-2002 (TREMBLref. 20, Last sequence update)  
 DE HYPOTHETICAL Protein RSC0848.  
 GN RSP0848 OR RS06110  
 OS *Ralstonia solanacearum* (*Pseudomonas solanacearum*)  
 OC Bacterium; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 Burkholderiaceae; Ralstonia.  
 OX NCBI\_TaxID=305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GM1000;  
 RX MEDLINE=21681879; PubMed=11823852;  
 RA Arlat M., Billault A., Brottier P., Artiguenave F., Gouzy J., Mangenot S.,  
 Chandler M., Choisne N., Claude-Renard C., Cattolico L.,  
 Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
 Signier P., Thebault P., Whalen M., Wincker P., Levy M.,  
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*."  
 RL Nature 415:477-502 (2002).  
 DR EML: A1646051; CAD1450.1;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 62 AA; 678 MW;  
 3AAC89CAC50144F3 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 62;  
 Best Local Similarity 100.0%; Fred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YVAD 4  
 Db 46 YVAD 49

RESULT 10  
 Q8XSA4 PRELIMINARY; PRT; 62 AA.  
 ID Q8XSA4;  
 AC Q8XSA4;  
 DT 01-MAR-2002 (TREMBLref. 20, Created)  
 DT 01-MAR-2002 (TREMBLref. 20, Last sequence update)  
 DE HYPOTHETICAL protein RSP0574.  
 GN RSP0574 OR RS06111  
 OS *Ralstonia solanacearum* (*Pseudomonas solanacearum*)  
 OC Bacterium; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 Burkholderiaceae; Ralstonia.  
 OX NCBI\_TaxID=305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21681879; PubMed=11823852;  
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
 Chandler M., Choisne N., Claude-Renard C., Cattolico L.,  
 Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
 Signier P., Thebault P., Whalen M., Wincker P., Levy M.,  
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*."  
 RL Nature 415:477-502 (2002).  
 DR EML: A1646051; CAD1450.1;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 62 AA; 678 MW;  
 3AAC89CAC50144F3 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 62;  
 Best Local Similarity 100.0%; Fred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YVAD 4  
 Db 46 YVAD 49

RESULT 11  
 Q89DP2 PRELIMINARY; PRT; 65 AA.  
 ID Q89DP2;  
 AC Q89DP2;  
 DT 01-JUN-2003 (TREMBLref. 24, Created)  
 DT 01-JUN-2003 (TREMBLref. 24, Last sequence update)  
 DE BS17397 protein.  
 GN  
 OS Bradyrhizobium japonicum.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 Bradyrhizobiaceae; Bradyrhizobium.  
 OX NCBI\_TaxID=375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USA 110;  
 RX MEDLINE=22484988; PubMed=12597275;  
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,  
 RA Sasamoto S., Watanabe A., Idesawa K., Iriuchi M., Kawashima K.,  
 RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,  
 RA Tabata S.;  
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
 Bradyrhizobium japonicum USDA110.";  
 RL DNA Res. 9:189-197 (2002).  
 DR EML: APO05962; BA052662.1;  
 RW Complete proteome.  
 SQ SEQUENCE 65 AA; 7091 MW; 4D8D7C3P9145F7B9 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 65;  
 Best Local Similarity 100.0%; Fred. No. 4.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YVAD 4  
 Db 46 YVAD 49

RESULT 12  
 Q9R5X3 PRELIMINARY; PRT; 66 AA.  
 ID Q9R5X3;  
 AC Q9R5X3;  
 DT 01-MAY-2000 (TREMBLref. 13, Created)  
 DT 01-MAY-2000 (TREMBLref. 13, Last sequence update)  
 DE Penicillin-binding protein 2B.  
 GN RSP0574 OR RS06111.  
 OS *Ralstonia solanacearum* (*Pseudomonas solanacearum*).  
 OC Bacterium; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 Burkholderiaceae; Ralstonia.  
 OX NCBI\_TaxID=305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9350888; PubMed=8071243;  
 RA Arlat M., Billault A., Brottier P., Artiguenave F., Gouzy J., Mangenot S.,  
 Chandler M., Choisne N., Claude-Renard C., Cattolico L.,  
 Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
 RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,  
 RT "Penicillin-binding protein 2B of *Streptococcus pneumoniae* in  
 piperacillin-resistant laboratory mutants.";  
 RL J. Bacteriol. 176:5574-5577 (1994).

DR GO; GO:0008658; P:penicillin binding; IEA.  
 DR GO; GO:00273; P:cell wall biosynthesis (sensu Bacteria); IEA.  
 DR InterPro:IPR001460; Transpeptidase.  
 DR Pfam:PF00905; Transpeptidase; 1.  
 FT NON-TER 1  
 FT 66 66  
 SQ SEQUENCE 66 AA; 7089 MW; 673DA1BCEC74B980 CRC64;  
 Query Match 100.0%; Score 21; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YYAD 4  
 Db 8 YYAD 11

RESULT 13  
 ID P79275; PRELIMINARY; PRT; 66 AA.  
 AC P79275;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Rho A (Fragment).  
 OS Sus scrofa (Pig).  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 OC NCBI\_TaxID:9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=domestic; TISSUE=Bulmonary vein;  
 RX MEDLINE=97040692; PubMed=886602;  
 RA Nishimura J., Sakihara C., Zhou Y., Kanaike H.;  
 RT "Expression of Rho A and Rho-kinase mRNAs in Porcine Vascular Smooth  
 Muscle.", Biochim. Biophys. Res. Commun. 227:750-754 (1996).  
 RL EMBL: D89499; BAA1396.1; -.  
 DR PIR; PC4222; PC4222.  
 DR HSSP; P06743; 1FTN.  
 DR GO; GO:0005525; P:GTP binding IEA.  
 DR GO; GO:0005925; P:small monomeric GTPase activity; IEA.  
 DR GO; GO:0007264; P:small monomeric GTPase mediated signal transduction; IEA.  
 DR InterPro:IPR001806; Ras\_transfrrmng.  
 DR Pfam; PF00071; ras; 1.  
 KW GTP-binding.  
 FT NON-TER 1 1  
 FT NON-TER 66 66  
 SQ SEQUENCE 66 AA; 7562 MW; 3BC71B220AD67C30 CRC64;  
 Query Match 100.0%; Score 21; DB 6; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YYAD 4  
 Db 7 YYAD 10

RESULT 14  
 ID Q8SP36; PRELIMINARY; PRT; 66 AA.  
 AC Q8SP36;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE MHC class II antigen (Fragment).  
 GN PYPA1.10.  
 OS Pygoscelsis papua (Gento Penguin).  
 OC Pygoscelsis; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Sphenisciformes; Spheniscidae;  
 OC Pygoscelsis.  
 OC NCBI\_TaxID:30457;

RN [1]  
 SEQUENCE FROM N.A. PubMed=11797106;  
 RX MEDLINE=21655119;  
 RA Tsuda T.T., Tauda M., Naruse T., Kawata H., Ando A., Shiina T.,  
 RA Fukuda M., Kurita M., Lemaho I., Kulski J.K., Inoko H.;  
 RT "Phylogenetic analysis of Penguin (Spheniscidae) species based on  
 RT sequence variation in MHC class II genes";  
 RL Immunogenetics 55:712-716 (2001).  
 DR EMBL; AB04359; BAB8630.1;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0045012; P:MHC Class II receptor activity; IEA.  
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.  
 DR GO; GO:0019816; P:antigen processing, exogenous antigen via M. . . ; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR003328; MHC-II\_beta; 1.  
 DR Pfam; PF00969; MHC-II\_beta; 1.  
 DR ProDom; PD0000328; MHC-II\_beta; 1.  
 KW Glycoprotein; MHC II; Transmembrane.  
 FT NON-TER 66 66  
 SQ SEQUENCE 66 AA; 7774 MW; A955PF9736710EADF CRC64;  
 Query Match 100.0%; Score 21; DB 7; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YYAD 4  
 Db 29 YYAD 32

RESULT 15  
 ID Q8SP52; PRELIMINARY; PRT; 66 AA.  
 AC Q8SP52;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Major histocompatibility complex (Fragment).  
 GN PYANL.01.  
 OS Pygoscelsis antarctica (Chinstrap penguin).  
 OC Pygoscelsis; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Sphenisciformes; Spheniscidae;  
 OC Pygoscelsis.  
 RN [1]  
 RP SEQUENCE FROM N.A. PubMed=11797106;  
 RX MEDLINE=21655119;  
 RA Tsuda T.T., Tauda M., Naruse T., Kawata H., Ando A., Shiina T.,  
 RA Fukuda M., Kurita M., Lemaho I., Kulski J.K., Inoko H.;  
 RT "Phylogenetic analysis of Penguin (Spheniscidae) species based on  
 RT sequence variation in MHC class II genes";  
 RL Immunogenetics 55:712-716 (2001).  
 DR EMBL; AB043556; BAB86820.1;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0045012; P:MHC Class II receptor activity; IEA.  
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.  
 DR GO; GO:0019816; P:antigen processing, exogenous antigen via M. . . ; IEA.  
 DR InterPro; IPR000333; MHC-II\_beta.  
 DR Pfam; PF00695; MHC-II\_beta; 1.  
 DR ProDom; PD000328; MHC-II\_beta; 1.  
 KW Glycoprotein; MHC II; Transmembrane.  
 FT NON-TER 66 66  
 SQ SEQUENCE 66 AA; 7839 MW; B41AD0CB0029FDC7 CRC64;  
 Query Match 100.0%; Score 21; DB 7; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YYAD 4

Db 29 YVAD 32  
Search completed: May 24, 2004, 14:41:00  
Job time : 38.5 secs

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OM protein - protein Search, using SW mode!

Run on: May 24, 2004, 14:36:17 ; Search time 51 Seconds  
 (without alignments)  
 22.161 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21 DDEV 4

Sequence: BLOSUM62 Gapo 10.0 , Gapext 0.5

Scoring table: 282547505 residues

Searched: 1586107 seqs, 282547505 residues

total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneset\_29Jan04 \*

1: GenesetDP1980s:  
 2: GenesetQP1980s:  
 3: GenesetQP2000s:  
 4: GenesetDP2001s:  
 5: GenesetQP2002s:  
 6: GenesetQP2003as:  
 7: GenesetQP2003bs:  
 8: GenesetQP2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	4 2 AAW06250	Aaw06250 ICE peptide
2	21	100.0	4 2 AAW76200	Aaw76200 Mouse caspase
3	21	100.0	4 2 AAW52756	Aaw52756 Aminomech
4	21	100.0	4 2 AAW48940	Aaw48940 Apopain
5	21	100.0	4 2 AAW56305	Aaw56305 Peptide C
6	21	100.0	4 2 AAW48948	Aaw48948 Apopain
7	21	100.0	4 2 AAY15622	Aay15622 Peptide u
8	21	100.0	4 2 AAY04114	Aay04114 Enzyme co
9	21	100.0	4 2 AAW68554	Aaw68554 Apopain a
10	21	100.0	4 2 AAY24411	Aay24411 Caspase p
11	21	100.0	4 2 AAW99676	Aaw99676 Caspase r
12	21	100.0	4 2 AAW94093	Aaw94093 Pro tease
13	21	100.0	4 3 AAY78347	Aay78347 Caspase 1
14	21	100.0	4 3 AAY69646	Aay69646 Caspase 1
15	21	100.0	4 3 AAY99958	Aay99958 Tetrapeptidase
16	21	100.0	4 3 AAB22889	Aab22889 Caspase 3
17	21	100.0	4 3 AAY49940	Aay49940 Synthetic
18	21	100.0	4 3 AAY79040	Aay79040 Caspase i
19	21	100.0	4 3 AAY88373	Aay88373 Peptide u
20	21	100.0	4 3 AAY83395	Aay83395 DEVD peptide
21	21	100.0	4 3 AAB226851	Aab226851 Synthetic
22	21	100.0	4 3 AAY80786	Aay80786 Fluorophore
23	21	100.0	4 3 AAO17431	Aao17431 Caspase 3
24	21	100.0	4 3 AAY69866	Aay69866 PARP cleavage
25	21	100.0	4 3 AAB10870	Aab10870 Aminocoumarin

## ALIGNMENTS

RESULT 1			
ID	AAW06250	standard; peptide: 4 AA.	
XX	AAW06250;		
AC			
XX		DT 03-MAR-1997 (first entry)	
XX		DE ICE peptide substrate.	
XX		XX Mch2; Ced-3/Ice; cysteine protease; apoptosis; autoimmune disease; XX cancer; HIV; Alzheimer's disease; therapy.	
XX		XX OS synthetic.	
XX		XX PN WO9636698-A1.	
PD		XX 21-NOV-1996.	
XX		XX 21-NOV-1996.	
PP		PP 16-MAY-1996;	96W0-US007010.
XX		PR 18-MAY-1995;	95US-00446925.
XX		PA (UYJE-) UNIV JEFFERSON THOMAS.	
XX		XX Litwack G, Alnemri ES, Fernandez-Alnemri T;	
XX		XX WPI: 1997-012077/01.	
XX		XX New isolated apoptotic cysteine protease, Mch 2 - used to develop prods. for use as anti-apoptotic agents or as cytotoxic agents.	
PT		PT	PT Disclosure, Page 28, 43PP; English.
XX		XX	XX A tetrapeptide (AAW06250) represents a site present in poly(ADP-ribose) that is cleaved by an interleukin-1 beta converting enzyme (ICE)-like protein during apoptosis. Another tetrapeptide (AAW06453) is the ICE cleavage site in pro-interleukin-1 beta. The 2 peptides were used to test the activity of human Ccp32, ICE and 2 isoforms alpha (see also AAW0644) and beta (AAW0645), of novel human apoptotic cysteine protease Mch2. Enzymatic activities were studied in total bacterial extracts from cells expressing these enzymes as GST fusion proteins. Neither Mch2 alpha nor Mch2 beta was able to cleave the YVAD substrate. Mch2 alpha, but not Mch2 beta, cleaved the DEVD substrate, but was 150-fold less active than CPP32.
SQ		SQ Sequence 4 AA;	

Query Match Similarity 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Best Local Matched Score 21; DB 2; Length 4;

AAW52756 standard; peptide; 4 AA.  
D X

matrices	*	observative	U;	mismatches	U;	models	U;	gaps	U;
Y	1	DEVD	4						
b	1		1						

RESULT 2  
AVW76200 standard; protein; 4 AA.  
D

A AAN76200;  
C  
X 26-NOV-1998 (first entry)  
X Mouse caspase I peptide motif #2.  
X  
X Caspase; thymocyte; inhibitor; immature; treatment; cancer; autoreactive;  
X leukaemia; melanoma; autoimmune disease; apoptosis; T cell;  
X receptor; infection; inflammatory disease; neurodegenerative disorder.

Mus sp. W09836057-A1

20-AUG-1998. 98WO-US003524.  
17-FEB-1998; 97US-00802474.  
18-FEB-1997; 97US-0094124.  
09-OCT-1997; (DAND ) DANA BARBER CANCER INST INC.  
(PROC-) PROCEPT INC.  
Reinherz E, Clayton L, Ocain TD, Patch RJ;

WPI: 1998-520756/44.

Identifying agents which inhibit or enhance caspase activity - and which may be used, e.g., in treatment of cancer or autoimmune diseases.

Disclosure: Page 8; 62pp; English.

AIW76198-W76202 are peptides used in a method for identifying an agent which inhibits a caspase expressed in immature thymocytes. Such agents may be used in the treatment of cancers (such as leukaemia or melanomas) and autoimmune diseases. Inhibition of apoptosis can result in the inhibition of lymphocyte down regulation, resulting in a T cell receptor population with an increased proportion of autoreactive T cells, i.e., an increased occurrence of T cells which have specificity for the host animal's own cells (e.g. cancer cells). By the same token, increasing the activity of the caspase enzyme enhances apoptosis of self-recoginising T cells, resulting in a decrease in the population of T cells which are responsible for autoimmune diseases. The compounds may also be useful in treating infections, inflammatory diseases and neurodegenerative diseases.

Sequence 4 AA;		Query Match	100.0%	Score 21;	DB 2;	Length 4;
		Best Local Similarity	100.0%	Pred. No.	1.4e+06;	
		Matches 4;	Conservative	Mismatches 0;	Indels 0;	Gaps 0;
disorders	2					

1 DEVD 4  
1 DEVD 4  
1 DEVD 4

RESULT 3  
HW52756

Memory - Counter		Unit	Value	Unit	Memory
1	X	GB	234529	-A.	GB
2	N				
3	X				
4	D				
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AA (MERK ) MERCK & CO INC.  
XX Chapman KT, Nicholson D, Rano T, Thornberry N;  
XX WPI: 1998-52384/45.  
XX  
XX New tetrapeptide coumarin derivatives - useful in combinatorial  
XX to identify substrate specificity of cysteine or serine proteases.  
XX

Claim 3; Page 42; 49pp; English.

The peptide is a specifically claimed example of new aminometacoumarin-labelled tetrapeptides of formula Ac-Xaa-Xaa-Xaa-App. These peptides are used to generate a fluorescent positional scanning combinatorial library for the investigation of the specificity of cysteine and serine proteases, e.g. in the analysis of interleukin-1 beta converting enzyme substrate and other caspase substrates, and to identify inhibitors which may mediate inhibition. The library preferably comprises a mixture of at least 200 of

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C tetrapptides
X
Q Sequence 4 AA:
Y Query Match Similarity 100.0%; Score 21; DB 2; Length 4;
Best Local Matches 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0
1 DEVD 4

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disorders

Sequence 4 AA;

	Query Match	Score 21;	DB 2;	Length 4;
Best Local Similarity	100.0%	Pred. No. 1.4e+06;		
Matches 4;	100.0%	Mismatches 0;		
Conservative		Indels 0;		
		Gaps 0;		

1 DEVD 4  
1 DEVD 4  
1 DEVD 4

RESULT 3  
HW52756

THEORY AND PRACTICE IN THE FIELD OF INTEGRATED MARKETING COMMUNICATIONS 13

4-phosphono(difluoromethyl) phenylalanine group; osteoporosis.

OS Synthetic.

XX OS Synthetic.

XX Synthetic.

XX Location/Qualifiers

1 /note= "N-terminal acetyl"

FT Modified-site

4 /note= "Optional attachment to aldehydes or ketones"

FT Modified-site

XX /note= "Optional attachment to aldehydes or ketones"

FT 14-MAY-1998.

XX PF 03-NOV-1997;

XX PR 04-NOV-1996;

XX PA (MERI ) MBRCK FROSST CANADA INC.

XX PI Desmarais S, Friesen R, Zamboni R;

XX DR 1998-34810/30.

XX Peptide(s) useful in binding assays for tyrosine phosphatases or cysteine proteases - contain two or more 4-Phosphono(difluoromethyl) phenylalanine groups to improve binding affinity.

XX Example: Page 29; 59pp; English.

CC Variants of the apopain (caspase-3) peptide substrate can be used as ligands for the binding assay used in the invention. The invention provides a method for use in a scintillation proximity binding assay (SPA) for proteases and phosphatases. The method involves using mutated proteases and phosphatases whereby the catalytic cysteine residue of the enzymes are replaced with a serine or alanine residue to correct the problem of interference in SPA from extraneous oxidising and alkylating agents. The mutation affects the catalytic properties of the enzyme but does not affect their binding properties. The invention claims for new ligands for use in SPA which have increased binding affinity for a tyrosine phosphatase or cysteine protease. The ligands contain at least two 4-phosphono(difluoromethyl) phenylalanine groups which increase binding affinity of the ligand to its respective enzyme. The assay can be used to determine the ability of new ligands and compound mixtures to competitively bind with an enzyme. The method is claimed to allow a better usage of SPA in the discovery of compounds for the treatment and study of diseases, e.g. diabetes, cancer and osteoporosis.

XX Sequence 4 AA;

CC Query Match 100.0%; Score 21; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OS Synthetic.

CC Qy 1 DEVD 4

Db 1 DEVD 4

XX RESULT 6

AAW48948

ID AAW48948 standard; protein; 4 AA.

XX Qy 1 DEVD 4

Db 1 DEVD 4

XX DE AAW48948;

XX DT 26-OCT-1995 (first entry)

XX DE Apopain (caspase-3) peptide substrate.

XX DE Apopain; caspase-3; protease; SPA; tyrosine phosphatase;

XX KW scintillation proximity binding assay; diabetes; cancer;

XX KW 4-phosphono(difluoromethyl) phenylalanine group; osteoporosis.

XX SQ Sequence 4 AA;

CC Query Match 100.0%; Score 21; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OS Synthetic.

CC Qy 1 DEVD 4

Db 1 DEVD 4

XX RESULT 5

AAW56305

ID AAW56305 standard; peptide; 4 AA.

XX AC AAW56305;

XX DT 22-JUL-1998 (first entry)

XX DE Peptide cleaved by interleukin-1-beta-converting enzyme-like protein.

XX KW N-acetyl-DEVD-methyl coumarinamide; MCA;

XX interleukin-1- beta-converting enzyme-like activity; ICE activity;

XX cysteine protease; investigation; substrate specificity.

OS Synthetic.

XX OS Synthetic.

XX PN JP10099075-A.

XX PN 21-APR-1998.

XX PD 30-SEP-1996; 96JP-00276813.

XX PR 30-SEP-1996; 96JP-00276813.

XX (SHIS ) SHISEIDO CO LTD.

XX PA WPI; 1998-289868/26.

XX PT Protein with interleukin-1-beta converting enzyme-like activity - useful in investigation of substrate specificity in, e.g. Parkinson's disease.

XX Disclosure: Page 2; 5pp; Japanese.

XX PS

XX Disclosure: Page 2; 5pp; Japanese.

XX The present sequence, N-acetyl-DEVD-methyl coumarinamide (MCA), CC represents a sequence that is cleaved by a protein with interleukin-1- beta converting enzyme (ICE)-like activity. The protein, which is obtained from human keratinocytes, has a relative molecular weight of 80 kDa. The ICE protein is part of the cysteine protease family and is useful for investigation of the mechanism of substrate specificity (e.g. Alzheimer's disease, Parkinson's disease, autoimmune disease, lymphoma, cancer and apoptosis).

XX SQ Sequence 4 AA;

CC Query Match 100.0%; Score 21; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 DEVD 4

CC Db 1 DEVD 4

XX RESULT 6

XX AAW48948

XX ID AAW48948 standard; protein; 4 AA.

XX Qy 1 DEVD 4

XX Db 1 DEVD 4

XX AC AAW48948;

XX DT 26-OCT-1995 (first entry)

XX DE Apopain (caspase-3) peptide substrate.

XX KW Apopain; caspase-3; protease; SPA; tyrosine phosphatase;

XX KW scintillation proximity binding assay; diabetes; cancer;

XX KW 4-phosphono(difluoromethyl) phenylalanine group; osteoporosis.

XX SQ Sequence 4 AA;

CC Query Match 100.0%; Score 21; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OS Synthetic.

CC Qy 1 DEVD 4

CC Db 1 DEVD 4

XX Key Modified-site 1

XX FT FT /note= "N-terminal acetyl"

XX FT FT /note= "Optional attachment to aldehydes or ketones"

XX PR WO9820156-A1.

XX PN 14-MAY-1999.

XX PD 03-NOV-1997; 97WO-CA000825.

XX PR 04-NOV-1996; 96US-0030408P.

XX PA (MERI ) MERCK FROSST CANADA INC.

XX XX Desmarais S, Friesen R, Gresser M, Kennedy B, Nicholson D;

XX PR Ramachandran C, Skorey K, Ford-Hutchinson A;

XX DR WPI; 1998-348103/30.  
 XX PT Enzyme binding assay for detection of useful compounds - uses mutant form  
 PT of wild-type enzyme, in which serine replaces cysteine at active site, to  
 PT reduce interference from oxidising/alkylating agents.  
 XX PS Example; Page 28; 63pp; English.  
 XX CC Variants of the apopain (caspase-3) peptide substrate can be used as  
 CC ligands for the binding assay used in the invention. The invention claims  
 CC for a method for use in a scintillation proximity binding assay (SPA) for  
 CC proteases and phosphatases. The method involves using mutated proteases  
 CC and phosphatases whereby the catalytic cysteine residue of the enzymes  
 CC are replaced with a serine or alanine residue to correct the problem of  
 CC interference in SPA from extraneous oxidizing and alkylating agents. The  
 CC mutation affects the catalytic properties of the enzyme but does not  
 CC affect their binding properties. The invention provides new ligands for  
 CC use in SPA which have increased binding affinity for a tyrosine  
 CC phosphatase or cysteine protease. The ligands contain at least two 4-  
 CC phosphono(difluoromethyl) phenylalanine groups which increase binding  
 CC affinity of the ligand to its respective enzyme. The assay can be used to  
 CC determine the ability of new ligands and compound mixtures to  
 CC competitively bind with an enzyme. The method is claimed to allow a  
 CC better usage of SPA in the discovery of compounds for the treatment and  
 CC study of diseases, e.g. diabetes, cancer and osteoporosis

XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 7  
 AAY15622  
 ID AAY15622 standard; peptide; 4 AA.

XX  
 AC AAY15622;  
 XX  
 DT 27-JUL-1999 (first entry)

XX DB Peptide used to make fluorescent reporter molecules.

XX KW Fluorogenic fluorescent reporter molecule; enzyme substrate; apoptosis;  
 KW protease; peptidase; apoptosis cascade; cancer; chemotherapeutic agent;  
 KW cell death; viral protease activity.  
 XX OS Synthetic.  
 XX PN WO9918856-A1.  
 XX PD 22-APR-1999.  
 XX PF 09-OCT-1998; 98WO-US021231.  
 XX PR 10-OCT-1997; 97US-0061582P.  
 PR 03-MAR-1998; 98US-00033661.  
 XX PA (CYTO-) CYTOVIA INC.

XX PI Weber E, Cai SX, Keana JFW, Drews JA, Zhang H;

XX DR WPI; 1999-312448/26.

XX PT New fluorogenic or fluorescent reporter molecules.

XX PS Claim 3; Page 160; 202pp; English.

XX AAY15618-Y15759 represent peptides used to make the fluorogenic or  
 CC fluorescent reporter molecules of the invention. These molecules contain  
 CC a peptide moiety (e.g. present sequence) which acts as a substrate for  
 CC enzymes involved in apoptosis or protease or peptidase enzymes. The  
 CC compounds can be used as fluorogenic or fluorescent substrates for  
 CC enzymes. Depending on the peptide moiety used, the fluorescent molecules  
 CC can be used for detecting or measuring the activity of an enzyme involved  
 CC in the apoptosis cascade in cells; to determine whether a test compound  
 CC has an effect on an enzyme involved in the apoptosis cascade in cells  
 CC for determining the sensitivity of an animal with cancer to treatment  
 CC with chemotherapeutic agents or determining whether a test substance  
 CC inhibits, prevents, causes or enhances cell death of test cells; for  
 CC detecting or measuring the activity of a viral protease in cells; for  
 CC determining whether a test compound has an effect on the activity of a  
 CC viral protease in cells; and for measuring the activity or determining  
 CC whether a test substance has an effect on the activity of a protease or  
 CC peptidase in cells  
 XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 8  
 AAY04114  
 ID AAY04114 standard; peptide; 4 AA.

XX  
 AC AAY04114;

XX DT 15-JUN-1999 (first entry)

XX DE Enzyme component #2 caspase recognition sequence.

XX Cross-linked polypeptide assay; cross-linked enzyme component; cleavage;  
 HIV; protease cleavage site.  
 XX  
 OS Synthetic.  
 XX PN WO9906537-A1.  
 XX PD 11-FEB-1999.  
 XX PP 23-JUL-1998; 98WO-US015343.  
 XX PR 30-JUL-1997; 97US-00902766.  
 XX PA (BOEFL) BOEHRINGER MANNHEIM CORP.

XX Powell MJ, Khanna P, Eisenbeis SJ, Lingenfelter D, Tietze LF;

XX PI Manning W;

XX DR; 1999-190002/16.

XX PT New cross-linked enzyme components - which have inhibited ability to  
 PT complement with other enzyme components to form an active enzyme complex.  
 XX PS Example 10; Page 34; 56pp; English.  
 XX  
 CC The present invention describes a cross-linked enzyme component (A),  
 CC which: (i) has an inserted enzyme recognition site (ERS) in a polypeptide  
 CC of the component; and (ii) has at least one covalent intrachain cross-  
 CC link between amino acid side chains of the polypeptide. The component  
 CC forms an enzymatically active complex with a second enzyme component,  
 CC upon cleavage of the ERS, but is inhibited from forming this complex  
 CC prior to cleavage. The complex has enzymatic activity which is different  
 CC from that of beta-galactosidase. The component may be used for  
 CC measurement of substances in biological samples. It is especially useful

CC for measurement of enzymes (e.g. proteases, particularly viral, phosphatases, glycosidase, amidase and esterase) in clinical samples, or CC for measurement of target polynucleotides. Assay methods using the new CC components exhibit extremely low inherent background signals, due to reduction or inhibition of complementation of enzyme components prior to cleavage. The present sequence represents a peptide from an example of the present invention

XX SQ Sequence 4 AA;  
Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
Db 1 DEVD 4

RESULT 9  
AAW68554 standard; protein; 4 AA.  
ID AAW68554;  
XX AC AAW68554;  
XX DT 25-JAN-1999 (first entry)  
XX DE Apopain aldehyde-inhibitor peptide L-761191.  
XX Inhibitor; apopain; binding site; crystal structure; primer; PCR; amplification; Escherichia coli; apoptosis.  
XX OS Synthetic.  
XX PH Key  
PT Modified-site 1 Location/Qualifiers  
PT /note= "acylated N-terminus"  
PT Modified-site 4 /note= "contains C-terminal aldehyde group replacing carboxyl group"  
PT  
XX PN US5834228-A.  
XX PD 10-NOV-1998.  
XX PF 13-FEB-1997; 97US-00800007.  
XX PR 13-FEB-1997; 97US-00800007.

XX PA (MERI ) MERCK & CO INC.  
PA (MERI ) MERCK FROSST CANADA INC.  
XX PI Thornberry NA, Gallant M, Pazil KM, Nicholson DW, Peterson EP, Rasper DM, Labelle M, Vaillancourt JP, Rotonda J, Ruei R, Becker JW, Gareau Y, Gareau Y;  
WPI: 1999-008706/01.  
XX Identifying inhibitors of apopain by rational drug design - from ability to bind to the enzyme's substrate binding domain, potentially useful for inhibiting apoptosis, e.g. in treatment of acquired immune deficiency syndrome, autoimmune disease, infections etc.  
PS Claim 1; Col 29; 22pp; English.

XX The invention relates to the identification of inhibitors of apopain by designing and synthesising a potential inhibitor that will form non-covalent bonds with amino acids in the apopain substrate binding site, based upon the crystal structure co-ordinates of an apopain:acetyl-DEVD-CHO complex, testing it for apopain inhibition. Production of apopain for the binding studies comprises expression of the p17 and p12 subunits separately. This sequence represents an aldehyde-inhibitor of apopain designated L-761191. The apopain inhibitors are potentially useful for

CC inhibiting apoptosis  
XX SQ Sequence 4 AA;  
Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SQ 1 DEVD 4  
Qy 1 DEVD 4  
Db 1 DEVD 4

RESULT 10  
AAV24411  
ID AAY24411 standard; peptide; 4 AA.  
XX AC AAY24411;  
XX DT 20-SEP-1999 (first entry)  
XX DE Caspase processing site peptide #2 in aldehyde form.  
XX Human; caspase; anti-apoptosis; processing site; aldehyde; apoptosis; KW hepatitis; ischaemic cerebral disease; Alzheimer's disease; cancer; KW diarrhoea; bone marrow toxicity.  
XX CS Homo sapiens.  
OS Synthetic.  
XX PN JP11180B91-A.  
XX PD 06-JUL-1999.  
XX PF 25-DEC-1997; 97JP-00356757.  
XX PR 25-DEC-1997; 97JP-00356757.  
XX PA (DAUC ) DAIICHI PHARM CO LTD.  
XX DR WPI; 1999-439401/37.  
XX New anti-apoptosis agents - useful for treating hepatitis, ischaemic cerebral diseases and Alzheimer's disease.  
XX Claim 6; Page 6; 7pp; Japanese.

CC The present invention describes anti-apoptosis agent(s) containing human caspase and/or inhibitor(s) of its inducer(s), (especially human caspase-1, human caspase-3 and/or a human caspase-3 inducer), comprising delivery of caspase inhibitor into active type of human caspase inducer. Also describes are anti-apoptosis agent(s) containing modified protein comprising amino acid sequence around the processing site of caspase, especially aldehyde-Ala-Asp, and Glu-Ser-Met-Asp, especially Glu-Ser-Met-Asp, used for treatment of disease caused by especially Glu-Ser-Met-Asp, used for treatment of disease caused by apoptosis including hepatitis, ischaemic cerebral diseases, Alzheimer's disease, adverse reactions of bone marrow toxicity and diarrhoea due to CC disease, administration of anticancer agent, especially hepatitis. The agents (s) are useful for treating disease caused by apoptosis e.g. ischaemic cerebral diseases, Alzheimer's disease, adverse reactions of bone marrow toxicity and diarrhoea due to administration of anticancer agent, especially hepatitis.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DEVD 4  
Db 1 DEVD 4

RESULT 11  
 ID AAW94093 Standard; peptide; 4 AA.  
 XX AAW99676 Standard; peptide; 4 AA.  
 AC AAW99676; 03-JUN-1999 (first entry)  
 XX DT 22-APR-1999 (first entry)  
 DB Protease inhibitor z-DEVD-FMK.  
 XX ICE; ALS; SOD gene; interleukin-1 converting enzyme; mutant; cell death; amyotrophic lateral sclerosis; transgenic; ICE-like caspase; apoptosis; traumatic brain injury; TBI; neurological; neurodegenerative; kidney; heart disease; immune system; intestinal; aging; viral infection; AIDS; acquired immune deficiency syndrome; gene therapy; protease inhibitor.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX Synthetic.  
 XX Key  
 FT Location/Qualifiers  
 FT 1  
 FT /note= "N-benzylloxycarbonyl group is attached to Asp"  
 FT Modified-site  
 FT 4  
 FT /note= "a fluoromethylketone (FMK) group is attached to Asp"  
 FT Modified-site  
 FT 1  
 FT /note= "a fluoromethylketone (FMK) group is attached to Asp"  
 XX OS  
 PN WO9857664-A1.  
 XX Key  
 FT Location/Qualifiers  
 FT 1  
 FT /note= "N-benzylloxycarbonyl group is attached to Asp"  
 FT Modified-site  
 FT 4  
 FT /note= "a fluoromethylketone (FMK) group is attached to Asp"  
 XX OS  
 PN WO9857664-A1.  
 XX PD  
 PD 23-DEC-1998.  
 XX PR  
 PR 18-JUN-1998; 98WO-US0122716.  
 XX PA  
 PA 19-JUN-1997; 97US-0050242P.  
 XX PI  
 PI (YUAN/ ) YUAN J.  
 PA (FRIE/ ) FRIEGLANDER R M.  
 XX DR  
 DR 1999-095294/08.  
 XX PT  
 PT Treating amyotrophic lateral sclerosis (ALS) or ALS-like symptoms - PT comprises inhibiting interleukin-1 converting enzyme (ICE) by gene therapy, useful for treating central nervous system damage.  
 XX Example 8; Page 72; 96pp; English.  
 XX PS  
 PS The present invention describes: (A) cross-linked prodrug, which: (i) has an inserted enzyme recognition site (ERS) in a polypeptide of the prodrug and (ii) has at least one covalent intrachain cross-link between amino acid side chains of the polypeptide. The prodrug is converted to a therapeutically more effective form upon cleavage of the ERS. (B) cross-linked prodrug, which: (i) has an inserted ERS in a polypeptide of the CLM covalently bonded between amino acid side chains of the polypeptide. The CLM comprises an enzymatically cleavable site. The prodrug is converted to a activated form of the prodrug may have any desired biological activity, including activity in suppression of inflammatory or immunological activity, promotion of growth or a direct cytotoxic effect on target cells. Following cleavage of the ERS, the prodrug reassembles internally to form the therapeutic drug. In the activated form, the prodrugs are at least 10 times more effective than the prodrugs. The present sequence represents a peptide used in an example from the present invention.  
 XX SQ  
 SQ Sequence 4 AA;  
 XX Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 1 DEVD 4  
 XX Sequence 4 AA;  
 XX Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 1 DEVD 4

Db	1	DEVD	4
<b>RESULT 13</b>			
AA	AY78347		
ID	AY78347	standard; peptide; 4 AA.	
AC	AY78347;		
XX			
DT	05-MAY-2000	(first entry)	
DE	Caspase 1 peptide Dns-SS-DEVD-CHO.		
XX			
KW	Caspase; protein array; screening; biomolecular activity; proteomic;		
KW	drug development; biosensor; diagnosis.		
XX			
OS	Unidentified.		
XX			
Key		Location/Qualifiers	
PH		1	
FT		/note= "ASP is N-terminally modified to dany1-SS-Asp"	
FT		4	
FT		/note= "ASP is C-terminally modified to Asp-CHO"	
XX			
PN	WO200004332-A1.		
XX			
PD	27-JAN-2000.		
XX			
PF	14-JUL-1999;	99WO-US015971.	
XX			
PR	14-JUL-1998;	98US-00115455.	
XX			
PA	(ZYOMYX) INC.		
XX			
PI	Wagner P, Ault-Riche D, Nock S, Itin C;		
XX			
DR	2000-171289/15.		
XX			
PT	New arrays for analyzing components of a fluid sample, useful for drug development, functional proteomics, clinical diagnostics and biosensors.		
XX			
PS	Example 7; Page 55; 81pp; English.		
XX			
The present invention describes an array (1) of proteins comprising a substrate, at least one organic thinfilm on some or all of the substrate surface, and patches arranged in discrete, known regions on portions of the substrate surface covered by organic thinfilm. Each of the patches comprises a protein immobilised on the underlying organic thinfilm. The arrays can be used for screening proteins for their ability to interact with a component of a sample. They can also be used for assaying for protein-protein binding interactions or analytes. They can be used for drug development, proteomics, clinical diagnostics and biosensors. The present sequence represents a peptide used in the exemplification of the present invention.			
SQ	Sequence 4 AA;		
Query Match	100.0%	Score 21; DB 3; Length 4;	
Best Local Similarity	100.0%	Pred. No. 1.4e+06;	
Matches	4	Mismatches 0;	
		Indels 0; Gaps 0;	
Qy	1	DEVD	4
Db	1	DEVD	4
<b>RESULT 14</b>			
AA	AY69646		
ID	AY69646	standard; peptide; 4 AA.	
XX			
AC	AY69646;		
XX			
DT	08-MAY-2000	(first entry)	
<b>RESULT 15</b>			
AA	AY99958		

XX	Caspase inhibitor peptide #1.		
XX	Caspase inhibitor; nitrogen-containing bisphosphonate; apoptosis; bone resorption; gastro-intestinal adverse effect; osteoporosis; Paget's disease; bone fracture; osteomalacia; periodontal disease; osteolysis.		
XX	Synthetic.		
XX		Key	
		PH	Location/Qualifiers
		FT	/note= "Conjugated to a benzyl oxy carbonyl (Z) N-terminal blocking group"
		FT	4
		FT	/note= "Conjugated to a fluoromethyl keto (FMK) C-terminal blocking group"
		XX	
		PN	WO9966945-A1.
		XX	
		PD	29-DEC-1999.
		XX	
		PF	21-JUN-1999;
		XX	99WO-US013961.
		PR	24-JUN-1998;
		PR	15-JUL-1998;
		PR	06-AUG-1998;
		PR	02-SEP-1998;
		XX	98GB-00019126.
		PA	(MERCK & CO INC.
		XX	
		PI	Reszka AA;
		XX	
		DR	WPI: 2000-147177/13.
		XX	
		PT	Composition containing nitrogen-containing bisphosphonate and caspase inhibitor, for inhibiting bone resorption, especially treatment of osteoporosis.
		XX	
		PS	Claim 5; Page 22; 33pp; English.
		XX	
		PI	
		XX	
		DR	
		XX	
		PT	
		XX	
		PS	
		XX	
		CC	Sequences AAY69646-Y69647 represent caspase inhibitor peptides which may be used in a novel composition for the inhibition of bone resorption. The composition comprises a nitrogen-containing bisphosphonate, or its salt, and a caspase inhibitor (such as peptides AAY69646-Y69647). Bone resorption may also be inhibited by sequential administration of a nitrogen-containing bisphosphonate and a caspase inhibitor. The nitrogen-containing bisphosphonate inhibits bone resorption by triggering apoptosis of osteoclasts. Although the caspase inhibitor has no effect on this process, it does inhibit a similar apoptotic action of the bisphosphonate on epithelial cells in the gastro-intestinal tract. The bisphosphonate/caspase inhibitor composition is used to inhibit bone resorption in mammals, specifically for oral treatment of osteoporosis (cf any aetiology) and Paget's disease, but also in cases of osteomalacia, periodontal disease, periprosthetic osteolysis and bone fractures. The caspase inhibitor mitigates the adverse gastro-intestinal effects (e.g., oesophageal ulcers or oesophagitis), sometimes associated with oral administration of the bisphosphonate, resulting in safer treatment and better patient compliance.
		XX	
		SQ	Sequence 4 AA;
		Query Match	Score 21; DB 3; Length 4;
		Best Local Similarity	Pred. No. 1.4e-06;
		Matches	Mismatches 0;
			Indels 0; Gaps 0;
		Qy	1
		Db	1
<b>RESULT 16</b>			
AA	AY69646		
ID	AY69646	standard; peptide; 4 AA.	
XX			
AC	AY69646;		
XX			
DT	08-MAY-2000	(first entry)	

ID AAY99958 standard; peptide; 4 AA.  
 XX  
 AC AAY99958;  
 XX  
 DT 27-OCT-2000 (first entry)  
 XX  
 DE Tetrapeptide aldehyde which is a potent inhibitor of caspase-3.  
 KW Inhibitor; apoptosis; cardiac; cerebral ischemia; stroke;  
 KW type I diabetes; immune deficiency syndrome; HIV; AIDS; cerebral;  
 KW spinal chord trauma; injury; alloppecia; ageing; Parkinson's disease;  
 KW Alzheimer's disease; Down's syndrome; spinal muscular atrophy;  
 KW multiple sclerosis; neurodegenerative disorders; caspase;  
 KW gamma-ketoacid tetrapeptide; cysteine proteases.  
 XX  
 OS Unidentified.  
 XX  
 FH Key  
 FT Modified-site 1  
 FT /note= "N-terminal acetyl"  
 FT Modified-site 4  
 FT /note= "D(CHO)"  
 XX  
 PN WO20032620-A1.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PP 30-NOV-1999; 99WO-CA001145.  
 XX  
 PR 02-DEC-1998; 98US-0110567P.  
 XX  
 PA (MERCK ) MERCK FROSST CANADA & CO.  
 XX  
 PI Grimm BL, Renaud J, Aspiotis R, Bayly CI, Zamboni R, Black S;  
 XX  
 DR 2000-412282/35.  
 XX  
 PT New gamma-ketoacid tetrapeptide compounds having caspase-3 inhibiting  
 PT activity, useful for treating e.g. Parkinson's disease, organ damage  
 PT during transportation, alopecia and ageing.  
 XX  
 Disclosure: Page 4; 12pp; English.  
 XX  
 CC The present invention relates to gamma-ketoacid tetrapeptide compounds,  
 CC which have been found to inhibit caspase-3. Inhibition of caspase  
 CC activity is known to inhibit apoptosis. The present sequence is a  
 CC tetrapeptide aldehyde which is a very potent inhibitor of caspase-3. This  
 CC peptide was designed to mimic the caspase-3 recognition site (see  
 CC AA99957). Caspase-3 inhibitors may be used for treating cardiac and  
 CC cerebral ischemia/reperfusion injury (e.g. stroke), type I diabetes,  
 CC immune deficiency syndrome (e.g. HIV or AIDS), cerebral and spinal chord  
 CC trauma injury, alopecia, ageing, Parkinson's disease, Alzheimer's  
 CC disease, Down's syndrome, spinal muscular atrophy, multiple sclerosis and  
 CC neurodegenerative disorders. They may also be used for treating other  
 CC caspase-3 mediated diseases.  
 XX  
 SQ Sequence 4 AA:  
 Query Match 100.0%; Score 21; DB 3; Length 4;  
 Best Local Similarity 100.0%; Fred. No. 1.4e-06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 ||||  
 Db 1 DEVD 4

GenCore version 5.1.6  
(c) 1993 - 2004 Compugen Ltd.

OM Protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 16.5 Seconds

(without alignments)  
12.515 Million cell updates/sec

Title: US-09-765-105a-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

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2: /cgnd\_6/ptodata/2/iaa/5B/COMB.pep:\*

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5: /cgnd\_6/ptodata/2/iaa/PCFTUS/COMB.pep:\*

6: /cgnd\_6/ptodata/2/iaa/backfile1/pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	21	100.0	4	1	US-09-446-925-9	Sequence 9, Appli
2	21	100.0	4	2	US-08-800-00A-10	Sequence 10, Appli
3	21	100.0	4	2	US-09-146-921-9	Sequence 9, Appli
4	21	100.0	4	2	US-08-915-414A-1	Sequence 1, Appli
5	21	100.0	4	2	US-08-816-855-9	Sequence 9, Appli
6	21	100.0	4	2	US-08-712-828-2	Sequence 2, Appli
7	21	100.0	4	3	US-08-926-588-39	Sequence 39, Appli
8	21	100.0	4	3	US-08-802-981-2	Sequence 2, Appli
9	21	100.0	4	3	US-09-210-755-2	Sequence 2, Appli
10	21	100.0	4	3	US-09-167-921-42	Sequence 42, Appli
11	21	100.0	4	3	US-09-210-756-1	Sequence 1, Appli
12	21	100.0	4	3	US-08-761-488-3	Sequence 3, Appli
13	21	100.0	4	3	US-08-761-483-10	Sequence 10, Appli
14	21	100.0	4	3	US-09-323-733-42	Sequence 42, Appli
15	21	100.0	4	3	US-09-058-968-2	Sequence 2, Appli
16	21	100.0	4	3	US-09-130-123-2	Sequence 1, Appli
17	21	100.0	4	3	US-09-130-123-7	Sequence 7, Appli
18	21	100.0	4	3	US-09-130-123-12	Sequence 12, Appli
19	21	100.0	4	3	US-09-130-123-15	Sequence 15, Appli
20	21	100.0	4	3	US-09-317-952-5	Sequence 5, Appli
21	21	100.0	4	3	US-09-309-003-1	Sequence 1, Appli
22	21	100.0	4	3	US-08-869-218-81	Sequence 1, Appli
23	21	100.0	4	3	US-09-257-218-82	Sequence 81, Appli
24	21	100.0	4	3	US-09-311-760-81	Sequence 82, Appli
25	21	100.0	4	3	US-09-311-760-82	Sequence 82, Appli
26	21	100.0	4	3	US-09-291-692-71	Sequence 71, Appli
27	21	100.0	4	3	US-08-446-925-9	US-08-446-925-9

Query Match 100.0% ; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0% ; Pred. No. 3e+05; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

RESULT 2

Qy 1 DEV'D 4  
Db 1 DEV'D 4

US-08-800-007A-10  
; Sequence 10 Application US/08800007A  
; Patent No. 5834228

GENERAL INFORMATION:  
; APPLICANT: Becker, Joseph  
; APPLICANT: Nicholson, Donald  
; APPLICANT: Rotonda, Jennifer  
; APPLICANT: Thornberry, Nancy  
; APPLICANT: Fazil, Kimberly  
; APPLICANT: Gallant, Michael  
; APPLICANT: Gareau, Yves  
; APPLICANT: Labelle, Marc  
; APPLICANT: Peterson, Erin  
; APPLICANT: Rasper, Dita

TITLE OF INVENTION:  
; CRYSTAL STRUCTURE OF APOPAIN  
; TITLE OF INVENTION:  
; CRYSTAL STRUCTURE OF APOPAIN  
; NUMBER OF SEQUENCES: 14

ATTORNEY/AGENT INFORMATION:  
; ADDRESSSEE: JOSEPH A. COPPOLA - MERCK & CO., INC.  
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
; CITY: RAILWAY  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/800,007A  
; FILING DATE: 13-FEB-1997  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COPPOLA, JOSEPH A  
; REGISTRATION NUMBER: 38,413  
; REFERENCE/DOCKET NUMBER: 19644  
; TELEPHONE: 732-594-6734  
; TELEX:  
; FAX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-800-007A-10

Query Match Similarity 100.0%; Score 21; DB 2; Length 4;  
; Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEV'D 4  
Db 1 DEV'D 4

RESULT 3

Qy 1 DEV'D 4  
Db 1 DEV'D 4

US-08-915-414A-1  
; Sequence 1, Application US/08915414A  
; Patent No. 5916822

GENERAL INFORMATION:  
; APPLICANT: LANDRUM, ET AL.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR MONITORING APOPTOSIS  
; TITLE OF INVENTION: AND DISTINGUISHING APOPTOSIS FROM NECROSIS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MITCHELL ALTER, COULTER INTERN. CORP.  
; STREET: 11800 SW 147 AVE.  
; CITY: MIAMI  
; STATE: FLORIDA  
; COUNTRY: USA  
; ZIP: 33196

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB Storage  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Microsoft Word 6.0/95  
; CURRENT APPLICATION DATA:

US-08-915-414A-1  
; Sequence 1, Application US/08915414A  
; Patent No. 5916822

GENERAL INFORMATION:  
; APPLICANT: LANDRUM, ET AL.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR MONITORING APOPTOSIS  
; TITLE OF INVENTION: AND DISTINGUISHING APOPTOSIS FROM NECROSIS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MITCHELL ALTER, COULTER INTERN. CORP.  
; STREET: 11800 SW 147 AVE.  
; CITY: MIAMI  
; STATE: FLORIDA  
; COUNTRY: USA  
; ZIP: 33196

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB Storage  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Microsoft Word 6.0/95  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/915,414A  
 FILING DATE: 20-AUG-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/444,051  
 FILING DATE: 18-MAY-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MITCHELL B. ALTER  
 REGISTRATION NUMBER: 28,684  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: (305) 380-3636  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 STRANDEDNESS: single  
 TOPOLogy: linear  
 MOLECULE TYPE: Peptide  
 US-08-915-414A-1

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 5  
 US-08-896-885-9  
 Sequence 9, Application US/08896685  
 Patent No. 5985640  
 GENERAL INFORMATION:  
 APPLICANT: Litwack, Gerald  
 ALINMRI, Emad S.  
 APPLICANT: Fernandez-Alinmri, Teresa  
 CURRENT: Mch2, AN APOPTOTIC CYSTEINE  
 TITLE OF INVENTION: PROTEASE AND COMPOSITIONS FOR MAKING AND  
 TITLE OF INVENTION: METHODS OF USING THE SAME  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz &  
 ADDRESS: No. 598564018  
 STREET: One Liberty Place, 46th floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/896,885  
 FILING DATE: 18-JUL-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/446,925  
 FILING DATE: 18-MAY-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DeLuca, Mark  
 REGISTRATION NUMBER: 33,229  
 REFERENCE/DOCKET NUMBER: TTU-1508  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids

TOPOLogy: linear  
 MOLECULE TYPE: protein  
 US-08-896-885-9

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 6  
 US-08-712-878-2  
 Sequence 2, Application US/08712878  
 Patent No. 598563  
 GENERAL INFORMATION:  
 APPLICANT: Su, Michael  
 APPLICANT: Gu, Yong  
 APPLICANT: Livingston, David J.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DECREASING  
 TITLE OF INVENTION: IGF1 AND IFN- $\gamma$  GAMMA PRODUCTION BY ADMINISTERING AN ICE  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr.  
 STREET: 155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10020

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/712,878  
 FILING DATE: 12-SEP-1996  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haley Jr., James F.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: VPI/96-05  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-596-3000  
 TELEFAX: 212-596-9090  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLogy: linear  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 1  
 OTHER INFORMATION: /note= "aspartic acid is acetylated"  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 4  
 OTHER INFORMATION: /note= "aspartic acid carboxy  
 OTHER INFORMATION: terminus is reduced to an aldehyde"  
 US-08-712-878-2

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEV4  
Dv 1 DEV4

RESULT 7  
US-09-226-568-39  
; Sequence 39, Application US/09226568  
; GENERAL INFORMATION:  
; APPLICANT: Achermann, Elizabeth J.  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcussen, Eric G.  
; TITLE OF INVENTION: Antisense Modulation of No. 6001992a1 Anti-apoptotic  
; TITLE OF INVENTION: bcl-2-Related Proteins  
; FILE REFERENCE: ISPH-0337  
; CURRENT APPLICATION NUMBER: US/09/226-568  
; CURRENT FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: Description of Artificial Sequence: peptide  
US-09-226-568-39

Query Match 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Fred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEV4  
Dv 1 DEV4

RESULT 8  
US-08-802-981-2  
; Sequence 2, Application US/08802981  
; Patent No. 6037137  
; GENERAL INFORMATION:  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packerd, Beverly S.  
; TITLE OF INVENTION: Compositions for the Detection of Enzyme  
; NUMBER OF SEQUENCES: 231  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,981  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE DOCKET NUMBER: 016865-000300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-802-981-2

RESULT 9  
US-09-270-735-2  
; Sequence 2, Application US/09270735  
; Patent No. 6153591  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drew, John  
; APPLICANT: Wang, Yan  
; APPLICANT: Weber, Richard  
; TITLE OF INVENTION: Dipeptide Caspase Inhibitors and the Use Thereof  
; FILE REFERENCE: 1735.0010001  
; CURRENT APPLICATION NUMBER: US/09/270,735  
; CURRENT FILING DATE: 1999-03-16  
; EARLIER APPLICATION NUMBER: 60/078,051  
; EARLIER FILING DATE: 1998-03-16  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 2  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide  
US-09-270-735-2

Query Match 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Fred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEV4  
Dv 1 DEV4

RESULT 10  
US-09-167-921-42  
; Sequence 42, Application US/09167921A  
; Patent No. 6172216  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, QingQing  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPH-0324  
; CURRENT APPLICATION NUMBER: US/09/167,921A  
; CURRENT FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 42  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: caspase assay substrate

US-09-167-921-42

Query Match Score 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels  
Matches 4; Conservative 0; Mismatches 0; Indels 0

22y 1 DEVD 4  
22b 1 DEVD 4

RESULT 11  
JS-09-270-736-1  
Sequence 1, Application US/09270736  
Patent No. 6184210  
GENERAL INFORMATION:  
APPLICANT: Keana, John F.W.  
APPLICANT: Cai, Sui Xiong  
APPLICANT: Guastella, John  
APPLICANT: Yang, Wu  
APPLICANT: Drews, John A.  
APPLICANT: Weber, Eckhard  
TITLE OF INVENTION: Dipeptide Apoptosis Inhibitors and the Use  
FILE REFERENCE: 1735.0380002  
CURRENT APPLICATION NUMBER: US/09/270,736  
CURRENT FILING DATE: 1999-03-16  
EARLIER APPLICATION NUMBER: US 09/168,945  
EARLIER FILING DATE: 1998-10-09  
EARLIER APPLICATION NUMBER: US 09/061,676  
EARLIER FILING DATE: 1997-10-10  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Peptide

JS-09-270-736-1

Query Match Score 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels  
Matches 4; Conservative 0; Mismatches 0; Indels 0

22y 1 DEVD 4  
22b 1 DEVD 4

RESULT 12  
JS-08-761-483-3  
Sequence 3, Application US/08761483  
Patent No. 6204261  
GENERAL INFORMATION:  
APPLICANT: Batchelor, Mark J  
APPLICANT: Bebbington, David J  
APPLICANT: Bemis, Guy W  
APPLICANT: Friedman, Wolf H  
APPLICANT: Gillespie, Roger J  
APPLICANT: Golec, Julian MC  
APPLICANT: Gu, Yong  
APPLICANT: Laufer, David J  
APPLICANT: Livingston, David J  
APPLICANT: Matharu, Saroop S  
TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1 BETA  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/761,483  
 FILING DATE: 06-DEC-1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HALEY JR, James F  
 REGISTRATION NUMBER: 27,794  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: 212-596-9090  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDBNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 4  
 OTHER INFORMATION: /note= "aspartic acid is  
 OTHER INFORMATION: derivative with amino-4-methylcoumarin"  
 US-08-761-483-10

Query Match Score 100.0%; Score 21; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Gaps 0;

Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 14  
 US-09-323-743-42  
 Sequence 42, Application US/09323743  
 / Patent No. 614386  
 GENERAL INFORMATION:  
 / APPLICANT: Bennett, C. Frank  
 / APPLICANT: Dean, Nicholas M.  
 / APPLICANT: Nicholoff, Brett P.  
 / APPLICANT: Zhang, QingQing  
 TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
 FILE REFERENCE: ISPH-0368  
 CURRENT APPLICATION NUMBER: US/09/323,743  
 CURRENT FILING DATE: 1999-06-01  
 EARLIER APPLICATION NUMBER: 09/277,020  
 EARLIER FILING DATE: 1998-03-26  
 EARLIER APPLICATION NUMBER: 09/167,921  
 EARLIER FILING DATE: 1998-10-07  
 NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 42  
 LENGTH: 4

Query Match Score 100.0%; Score 21; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Gaps 0;  
 OTHER INFORMATION: Synthetic  
 US-09-323-743-42

Query Match Score 100.0%; Score 21; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Gaps 0;  
 OTHER INFORMATION: Artificial Sequence  
 OTHER INFORMATION: Synthetic  
 US-09-323-743-42

RESULT 15  
 US-09-058-969-2  
 / Sequence 2, Application US/09058969A  
 / Patent No. 6228603  
 / GENERAL INFORMATION:  
 / APPLICANT: Reed, John C.  
 / APPLICANT: Devereaux, Quian  
 / APPLICANT: Salvesen, Guy S.  
 / APPLICANT: Takahashi, Ryo-uke  
 / APPLICANT: Roy, Natalie  
 TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of  
 / Caspase Activity  
 FILE REFERENCE: LJ 3080  
 CURRENT APPLICATION NUMBER: US/09/058,969A  
 CURRENT FILING DATE: 1998-04-10  
 EARLIER APPLICATION NUMBER: 08/862,087  
 EARLIER FILING DATE: 1997-05-22  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 2  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Unknown  
 FEATURE:  
 OTHER INFORMATION: Description of Unknown Organism: Consensus Sequence  
 US-09-058-969-2

Query Match Score 100.0%; Score 21; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
 Db 1 DEVD 4

Search completed: May 24, 2004, 14:39:00  
 Job time : 17.5 secs

GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 Compugen Ltd.

## OM Protein - Protein search, using SW model

Run on: May 24, 2004, 14:39:37 ; Search time 38 Seconds  
 (without alignments)

29,360 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21 DEVD 4 Sequence: 1 DEVD 4

Scoring table: BLOSUM62 Gapext 0.5

Gapop 10.0 , Gapext 0.5

Searched: 1149313 seqs, 278921704 residues

## Total number of hits satisfying chosen parameters:

1149313

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing First 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	9 US-09-045-620-4	Sequence 4, Appli
2	21	100.0	4	9 US-09-734-846-42	Sequence 42, Appli
3	21	100.0	4	9 US-09-799-463-2	Sequence 2, Appli
4	21	100.0	4	9 US-09-735-363A-85	Sequence 85, Appli
5	21	100.0	4	9 US-09-799-995-2	Sequence 2, Appli
6	21	100.0	4	9 US-09-932-768-71	Sequence 71, Appli
7	21	100.0	4	9 US-09-856-754-11	Sequence 11, Appli
8	21	100.0	4	9 US-09-981-41-3	Sequence 3, Appli
9	21	100.0	4	9 US-09-737-255-1	Sequence 1, Appli
10	21	100.0	4	9 US-09-920-332-1	Sequence 8, Appli
11	21	100.0	4	9 US-09-845-028-8	Sequence 52, Appli
12	21	100.0	4	9 US-09-954-697-52	Sequence 5, Appli
13	21	100.0	4	9 US-09-387-787-5	Sequence 2, Appli
14	21	100.0	4	10 US-09-161-112-2	Sequence 7, Appli
15	21	100.0	4	10 US-09-866-512A-7	Sequence 6, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OTHER INFORMATION: Description of Artificial Sequence

FEATURE: caspase-specific peptide

NAME/KEY: MOD\_RES

LOCATION: (4)

OTHER INFORMATION: aminomethyl coumarin linked with residue 4

US-09-045-620-4

RESULT 1 ; Sequence 4, Application US/09045620-4

; Patent No. US20010005793A1

; GENERAL INFORMATION:

; APPLICANT: BJORNSTI, Mary-Ann

; APPLICANT: HALL, David

; APPLICANT: KANG, Jason

; TITLE OF INVENTION: MODULATORS OF EUKARYOTIC CASPASES

; FILE REFERENCE: 209855.002/2TUS

; CURRENT APPLICATION NUMBER: US/09/045,620

; CURRENT FILING DATE: 2000-03-20

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 4

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURER:

; OTHER INFORMATION: caspase-specific peptide

Sequence 42, Application US/09734846  
 GENERAL INFORMATION:  
 APPLICANT: Bennett, C. Frank  
 APPLICANT: Dean, Nicholas M.  
 APPLICANT: Monia, Brett P.  
 APPLICANT: Nickoloff, Brian J.  
 APPLICANT: Zhang, QingQing  
 TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
 FILE REFERENCE: ISPH-0528  
 CURRENT APPLICATION NUMBER: US/09/734,846  
 CURRENT FILING DATE: 2000-12-12  
 PRIOR APPLICATION NUMBER: 09/277,020  
 PRIOR FILING DATE: 1998-03-26  
 PRIOR APPLICATION NUMBER: 09/167,921  
 PRIOR FILING DATE: 1998-10-07  
 PRIOR APPLICATION NUMBER: 09/322,743  
 PRIOR FILING DATE: 1999-06-02  
 NUMBER OF SEQ ID NOS: 74  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 42  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-734-846-42

Query Match Similarity 100.0%; Score 21; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
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 Db 1 DEVD 4

RESULT 4  
 US-09-735-363A-85  
 Sequence 85, Application US/09735363A  
 Patent No. US20010041681A1  
 GENERAL INFORMATION:  
 APPLICANT: Filion, Mario  
 APPLICANT: Phillip, Nigel  
 TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
 FILE REFERENCE: 02811-0161  
 CURRENT APPLICATION NUMBER: US/09/735,363A  
 CURRENT FILING DATE: 2000-12-12  
 PRIOR APPLICATION NUMBER: 60/170,325  
 PRIOR FILING DATE: 1999-12-13  
 PRIOR APPLICATION NUMBER: 60/228,925  
 PRIOR FILING DATE: 2000-08-29  
 NUMBER OF SEQ ID NOS: 87  
 SOFTWARE: PatentIn Version 3.0  
 SEQ ID NO: 85  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic Peptide  
 US-09-735-363A-85

Query Match Similarity 100.0%; Score 21; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
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 Db 1 DEVD 4

RESULT 5  
 US-09-799-994-2  
 Sequence 2, Application US/09799994  
 Patent No. US2002009757A1  
 GENERAL INFORMATION:  
 APPLICANT: Reed, John C.  
 APPLICANT: Deveraux, Quinn  
 APPLICANT: Salvesen, Guy S.  
 APPLICANT: Takahashi, Ryosuke  
 APPLICANT: Roy, Natalie  
 TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of Apoptosis (IAP) Protein Regulation of Caspase Activity  
 FILE REFERENCE: LJ 3080  
 CURRENT APPLICATION NUMBER: US/09/599,994  
 CURRENT FILING DATE: 2001-03-05  
 PRIOR APPLICATION NUMBER: 09/058,969  
 PRIOR FILING DATE: 1998-04-10  
 PRIOR APPLICATION NUMBER: 08/862,087  
 PRIOR FILING DATE: 1997-05-22  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 2  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Unknown  
 FEATURE:  
 OTHER INFORMATION: Description of Unknown Organism:Consensus Sequence  
 US-09-799-994-2

Query Match Similarity 100.0%; Score 21; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
 ||||  
 Db 1 DEVD 4

RESULT 6

Sequence 43, Application US/09799946  
 GENERAL INFORMATION:  
 APPLICANT: Bennett, C. Frank  
 APPLICANT: Dean, Nicholas M.  
 APPLICANT: Monia, Brett P.  
 APPLICANT: Nickoloff, Brian J.  
 APPLICANT: Zhang, QingQing  
 TITLE OF INVENTION: For Agents That Alter Inhibitor of  
 FILE REFERENCE: ISPH-0529  
 CURRENT APPLICATION NUMBER: US/09/799,463  
 CURRENT FILING DATE: 2001-03-05  
 PRIOR APPLICATION NUMBER: 09/058,969  
 PRIOR FILING DATE: 1998-04-10  
 PRIOR APPLICATION NUMBER: 08/862,087  
 PRIOR FILING DATE: 1997-05-22  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 2  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Unknown  
 FEATURE:  
 OTHER INFORMATION: Description of Unknown Organism:Consensus Sequence  
 US-09-799-943-2

Query Match Similarity 100.0%; Score 21; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
 ||||  
 Db 1 DEVD 4

US-09-952-768-71  
Sequence 71, Application US/09952768  
Patent No. US200200315242A1

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.  
Fernandes-Alnemri, Teresa  
Litwack, Gerald  
Armstrong, Robert

ADDRESS: NUCLEIC ACIDS ENCODING AND METHODS OF USE

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEES: Seed Intellectual Property Law Group  
STREET: Suite 6300, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952,768

FILING DATE: 10-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Christiansen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 480140.424C4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-0331

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 71:

US-09-952-768-71  
Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

US-09-858-754-11

GENERAL INFORMATION:

APPLICANT: Johnson, Gary L.

TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS

FILE REFERENCE: CPI-042

CURRENT APPLICATION NUMBER: US/09/858,754

CURRENT FILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: 09/021,130

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: 60/039,740

PRIOR FILING DATE: 1997-02-14

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 11

LENGTH: 4

TYPE: PRT

ORGANISM: synthetic construct

US-09-858-754-11  
Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

Query Match 100.0%; Score 21; DB 9; Length 4;  
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Qy 1 DEVD 4

Db 1 DEVD 4

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DEVD 4

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DEVD 4

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DEVD 4

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

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Qy 1 DEVD 4

Db 1 DEVD 4

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

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Db 1 DEVD 4

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Qy 1 DEVD 4

Db 1 DEVD 4

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

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Qy 1 DEVD 4

Db 1 DEVD 4

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Best Local Similarity 100.0%; Pred. No. 1e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

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 Db 1 DEV4 1 ||| 1 |||

RESULT 10  
 US-09-910-312-1  
 Sequence 1, Application US/09920332  
 Patent No. US20020105631A1  
 GENERAL INFORMATION:  
 APPLICANT: Alnemri, Emad S.  
 TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES  
 FILE PREFERENCE: 4:80140.431D2  
 CURRENT APPLICATION NUMBER: US/09/954,697  
 CURRENT FILING DATE: 2001-09-14  
 NUMBER OF SEQ ID NOs: 116  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 52  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-09-954-697-52

Query Match 100.0%; Score 21; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
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Qy 1 DEV4 1 ||| 1 |||  
 Db 1 DEV4 1 ||| 1 |||

RESULT 13  
 US-09-947-387-5  
 Sequence 5, Application US/09947387  
 Patent No. US2002015085A1  
 GENERAL INFORMATION:  
 APPLICANT: Weber, Edward  
 APPLICANT: Cai, Sui Xiong  
 APPLICANT: Keana, John F.W.  
 APPLICANT: Drewe, John A.  
 APPLICANT: Zhang, Han-Zhong  
 TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecule  
 TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
 TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
 TITLE OF INVENTION: Use Thereof  
 FILE PREFERENCE: 1735.0290005

CURRENT APPLICATION NUMBER: US/09/947,387  
 CURRENT FILING DATE: 2001-09-07  
 PRIOR APPLICATION NUMBER: US 60/061,582  
 PRIOR FILING DATE: 1997-10-10  
 PRIOR APPLICATION NUMBER: US 60/115,746  
 PRIOR FILING DATE: 1998-03-03  
 PRIOR APPLICATION NUMBER: US 09/168,688  
 PRIOR FILING DATE: 1998-10-09  
 NUMBER OF SEQ ID NOS: 142  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 5  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 OTHER INFORMATION: Peptide  
 US-09-947-387-5

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 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14  
 US-09-161-172-2  
 Sequence 2, Application US/09161172  
 Publication No. US20030044776A1

Qy 1 DEV4 1 ||| 1 |||  
 Db 1 DEV4 1 ||| 1 |||

RESULT 12  
 US-09-954-697-52

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: GENERAL INFORMATION:
: APPLICANT: Dylens, James A.
: APPLICANT: Miller, Scott W.
: APPLICANT: Ghosh, Sunitra S.
: APPLICANT: Davis, Robert E.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
: AGENTS THAT ALTER MITOCHONDRIAL PERMEABILITY
: TITLE OF INVENTION: TRANSITION PORES
: FILE REFERENCE: 660088,418
: CURRENT APPLICATION NUMBER: US/09/1161,172
: CURRENT FILING DATE: 1998-09-25
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: Fast-SEQ for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 4
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: caspase-3 specific fluorogenic peptide substrate
US-09-1161-172-2

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Best Local Similarity 100.0%; Pred. No. 1e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DEVD 4
Db      1 DEVD 4

RESULT 15
US-09-866-512A-7
Sequence 7, Application US/09866512A
Publication No US20030033954A1
GENERAL INFORMATION:
APPLICANT: Meade, Thomas J
TITLE OF INVENTION: Magnetic Resonance Imaging Agents for the Detection of Physiology
TITLE REFERENCE: A-56634-7
CURRENT APPLICATION NUMBER: US/09/866,512A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/287,619
PRIOR FILING DATE: 2001-05-26
PRIOR APPLICATION NUMBER: US 08/460,511
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: US 08/486,968
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/971,855
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 09/134,072
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 09/866,512
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/405,046
PRIOR FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: US 60/063,328
PRIOR FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 4
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: could be from any mammal.

US-09-866-512A-7
Query Match          100.0%; Score 21; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DEVD 4
Db      1 DEVD 4

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: May 24, 2004, 14:38:22 ; Search time 175 Seconds

(without alignments)

22.310 Million cell updates/sec

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 Perfect score: 21  
 Sequence: 1 DBVD 4

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 Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 6019581

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Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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33: /cn2-6/ptodata/2/paa/US60 COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1  
 PCT/US00-02329-1  
 GENERAL INFORMATION:  
 1. APPLICANT: Cytovia, Inc.  
 2. TITLE OF INVENTION: Methods of Identifying Potentially Therapeutically Effective Antineoplastic Agents with Viable Cultured Cells Having an Intact Cell Membrane and Product by  
 3. TITLE OF INVENTION: Same  
 4. FILE REFERENCE: 1735.032PC02  
 5. CURRENT APPLICATION NUMBER: PCT/US00/02329  
 6. CURRENT FILING DATE: 2000-02-01  
 7. EARLIER APPLICATION NUMBER: 60/118,102  
 8. EARLIER FILING DATE: 1999-02-01  
 9. EARLIER APPLICATION NUMBER: 09/454,595  
 10. EARLIER FILING DATE: 1999-12-07  
 11. NUMBER OF SEQ ID NOs: 9  
 12. SOFTWARE: Patentin Ver. 2.1  
 13. SEQ ID NO: 1  
 14. LENGTH: 4  
 15. TYPE: PRT  
 16. ORGANISM: Artificial Sequence  
 17. FEATURE:

Result %  
 No. Score Match Length DB ID Description

; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
PCT-US00-02329-1

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Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DEVD 4  
Db 1 DEVD 4

RESULT 2  
PCT-US00-02332-1

Sequence 1, Application PC/TUS0002332  
; GENERAL INFORMATION:  
; APPLICANT: CYTOVIA, INC.  
; APPLICANT: CAL, SUI XIONG  
; APPLICANT: ZHENG, HAN-ZHONG  
; APPLICANT: WANG, YAN  
; APPLICANT: TSENG, BEN  
; APPLICANT: KASIBHATLA, SHAILAJA  
; APPLICANT: DREW, JOHN A.  
; TITLE OF INVENTION: GAMBOGIC ACID, ANALOGS AND DERIVATIVES AS ACTIVATORS OF  
; TITLE OF INVENTION: CASPASES AND INDUCERS OF APOPTOSIS  
; FILE REFERENCE: 1735\_012PC03  
; CURRENT APPLICATION NUMBER: PCT/US00/02332  
; CURRENT FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn Ver. 2.1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
PCT-US00-02332-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DEVD 4  
Db 1 DEVD 4

RESULT 3  
PCT-US00-09319-3

Sequence 3, Application PC/TUS0009319  
; GENERAL INFORMATION:  
; APPLICANT: Cytovia, Inc.  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Weber, Eckard  
; APPLICANT: Wang, Yan  
; APPLICANT: Mills, Goddon B.  
; APPLICANT: Green, Douglas R.  
; TITLE OF INVENTION: Caspase Inhibitors and the Use Thereof  
; FILE REFERENCE: 1735\_012PC02  
; CURRENT APPLICATION NUMBER: PCT/US00/09319  
; CURRENT FILING DATE: 2000-04-07  
; EARLIER APPLICATION NUMBER: US 60/128,545  
; EARLIER FILING DATE: 1999-04-09  
; EARLIER APPLICATION NUMBER: US 60/158,370  
; EARLIER FILING DATE: 1999-10-12  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Unknown Organism

RESULT 4  
PCT-US00-14451-42

Sequence 42, Application PC/TUS0014451  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, QingQing  
; APPLICANT: ISIS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPH-0460  
; CURRENT APPLICATION NUMBER: PCT/US00/14451  
; CURRENT FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 09/323,743  
; PRIOR FILING DATE: 1999-06-02  
; PRIOR APPLICATION NUMBER: 09/167,921  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 09/277,020  
; PRIOR FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 42  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
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; LENGTH: 4  
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; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; SEQ ID NO: 42  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Caspase

RESULT 5  
PCT-US01-04137-1

Sequence 1, Application PC/TUS0104137  
; GENERAL INFORMATION:  
; APPLICANT: ALEXION PHARMACEUTICALS, INC.  
; APPLICANT: Fodor, William L.  
; TITLE OF INVENTION: MIXTURES OF CASPASE INHIBITORS AND METHODS OF USE THEREOF  
; FILE REFERENCE: 1087-15PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/04137  
; CURRENT FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Caspase  
; OTHER INFORMATION: Inhibitor  
; OTHER INFORMATION: Inhibitor

PCT-US01-04137-1  
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 Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 6  
 PCT-US01-48256-1  
 Sequence 1, Application PC/TUS0148256  
 GENERAL INFORMATION:  
 APPLICANT: Regents of the University of Michigan  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING  
 TITLE OF INVENTION: PROTEOLYTIC ACTIVITY  
 FILE REFERENCE: 11203-003WO1  
 CURRENT APPLICATION NUMBER: PCT/US01/48256  
 CURRENT FILING DATE: 2001-12-13  
 PRIOR APPLICATION NUMBER: 09/737,255  
 PRIOR FILING DATE: 2000-12-13  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: FABSEQ for Windows Version 4.0  
 SEQ ID NO 1  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 PCT-US01-48256-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 7  
 PCT-US02-04060-52  
 Sequence 52, Application PC/TUS0204060  
 GENERAL INFORMATION:  
 APPLICANT: Massachusetts Institute of Technology, et al.  
 TITLE OF INVENTION: Peptides that Inhibit Poly-Glutamine Aggregation  
 FILE REFERENCE: M0656/7062WO (JRV)  
 CURRENT APPLICATION NUMBER: PCT/US02/04060  
 CURRENT FILING DATE: 2002-01-11  
 PRIOR APPLICATION NUMBER: US 60/267,898  
 PRIOR FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: US 60/334,891  
 PRIOR FILING DATE: 2001-11-15  
 NUMBER OF SEQ ID NOS: 52  
 SEQ ID NO 52  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Caspase Inhibitor  
 PCT-US02-04060-52

Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 8

PCT-US02-07569-1  
 Sequence 1, Application PC/TUS0207569  
 GENERAL INFORMATION:  
 APPLICANT: Cytovia, Inc.  
 TITLE OF INVENTION: Multifluoro-substituted Chalcones and Analogs as Activators of Apoptosis and the Use Thereof  
 FILE REFERENCE: 1735.054PC01  
 CURRENT APPLICATION NUMBER: PCT/US02/07569  
 CURRENT FILING DATE: 2002-02-14  
 PRIOR APPLICATION NUMBER: 60/275,473  
 PRIOR FILING DATE: 2001-03-14  
 NUMBER OF SEQ ID NOS: 1  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Fluorogenic Substrate  
 PCT-US02-07569-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 9  
 PCT-US02-14722-1  
 Sequence 1, Application PC/TUS0214722  
 GENERAL INFORMATION:  
 APPLICANT: Cytovia, Inc.  
 APPLICANT: Cai, Sui Xiong  
 APPLICANT: Kasibhatla, Shailaja  
 APPLICANT: Drew, John  
 APPLICANT: Reddy, P. Sarjeeva  
 APPLICANT: Zhang, Han-Zhong  
 TITLE OF INVENTION: Substituted N'-(Arylcarbonyl)-Benzhydrazides, N-(Arylcarbonyl)-Benzylidene-hydrazides And Analogs as Activators and Inducers of Apoptosis And The Use Thereof  
 FILE REFERENCE: 1735.056PC01  
 CURRENT APPLICATION NUMBER: PCT/US02/14722  
 CURRENT FILING DATE: 2002-05-10  
 PRIOR APPLICATION NUMBER: US 60/289,803  
 PRIOR FILING DATE: 2001-05-10  
 NUMBER OF SEQ ID NOS: 1  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Fluorogenic substrate  
 PCT-US02-14722-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 10  
 PCT-US2-15598-1  
 Sequence 1, Application PC/TUS0215598  
 GENERAL INFORMATION:  
 APPLICANT: CYTOVIA, INC.  
 APPLICANT: CAI, SUI XIONG

APPLICANT: XU, LIFEN  
 APPLICANT: STORER, RICHARD  
 APPLICANT: ATTARDO, GIORGIO  
 TITLE OF INVENTION: 7-B-FUSED 4H-CHROMENE AND ANALOGS AS ACTIVATORS OF CASPASES AND  
 FILE REFERENCE: 1735.065PC01  
 CURRENT APPLICATION NUMBER: PCT/US02/15398  
 CURRENT FILING DATE: 2002-05-16  
 PRIOR APPLICATION NUMBER: 60/290,976  
 NUMBER OF SEQ ID NOS: 1  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 1  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Fluorogenic substrate  
 PCT-US02-15398-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 13  
 PCT-US02-17108-1  
 Sequence 1, Application PC/TUS0217108  
 GENERAL INFORMATION:  
 APPLICANT: Cytovia, Inc.

APPLICANT: Cai, Sui Xiong  
 APPLICANT: Nguyen, Bao Ngoc  
 APPLICANT: Drewe, John  
 APPLICANT: Reddy, P. Sanjeeva  
 APPLICANT: Kasibhatla, Shailaja  
 APPLICANT: Pervin, Atra  
 TITLE OF INVENTION: 4-Substituted-1-(arylmethylidene)thiogemcarbazide,  
 4-Cai, Sui Xiong  
 TITLE OF INVENTION: 4-Substituted-1-(arylcarbonyl)thiogemcarbazide and  
 Analogs as Activators of Caspases and Inducers of  
 Apoptosis and the Use Thereof  
 TITLE OF INVENTION: 4-Substituted-1-(arylcarbonyl)thiogemcarbazide, and  
 Analogs as Activators of Caspases and Inducers of  
 Apoptosis and the Use Thereof  
 FILE REFERENCE: 1735.060PC01  
 CURRENT APPLICATION NUMBER: PCT/US02/17108  
 CURRENT FILING DATE: 2002-05-31  
 PRIOR APPLICATION NUMBER: US 60/294,641  
 NUMBER OF SEQ ID NOS: 1  
 SEQ ID NO: 1  
 LENGTH: 4  
 TYPE: PRT  
 FEATURE:  
 OTHER INFORMATION: Fluorogenic substrate

RESULT 11  
 PCT-US02-15401-1  
 Sequence 1, Application PC/TUS0215401  
 GENERAL INFORMATION:  
 APPLICANT: Cytovia, Inc.  
 APPLICANT: Shire BioChem, Inc.  
 APPLICANT: Cai, Sui Xiong  
 APPLICANT: Zhang, Hong  
 APPLICANT: Kmittz, William E.  
 APPLICANT: Jiang, Songchun  
 APPLICANT: Drewe, John A.  
 APPLICANT: Storer, Richard  
 TITLE OF INVENTION: Substituted Coumarins and Quinolines and Analogs as Activators of  
 Caspases and the Use Thereof  
 FILE REFERENCE: 1735.066PC01  
 CURRENT APPLICATION NUMBER: PCT/US02/15401  
 CURRENT FILING DATE: 2002-05-16  
 NUMBER OF SEQ ID NOS: 1  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 1  
 LENGTH: 4  
 TYPE: PRT  
 FEATURE:  
 OTHER INFORMATION: Fluorogenic substrate

Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 12  
 PCT-US02-15713-1  
 Sequence 1, Application PC/TUS0215713  
 GENERAL INFORMATION:  
 APPLICANT: BE CORPORATION (NY)  
 APPLICANT: YAN, Xiongwei  
 APPLICANT: MIRAGLIA, Sheri  
 APPLICANT: YUAN, Pau M  
 TITLE OF INVENTION: Substituted 4-Aryl-3-(3-Aryl-1-Oxo-2-Propenyl)-2(1H)-Quinolone

Query Match 100.0%; Score 21; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 14  
 PCT-US02-17486-1  
 Sequence 1, Application PC/TUS0217486  
 GENERAL INFORMATION:  
 APPLICANT: Cytovia, Inc.  
 APPLICANT: Cai, Sui Xiong  
 APPLICANT: Zhang, Han Zhong  
 APPLICANT: Drewe, John  
 APPLICANT: Kasibhatla, Shailaja  
 TITLE OF INVENTION: Substituted 4-Aryl-3-(3-Aryl-1-Oxo-2-Propenyl)-2(1H)-Quinolone

Job time : 176 sec

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TITLE OF INVENTION: Analogs as Activators of Caspases and Inducers of Apoptosis and  
FILE REFERENCE: 1735.057P01  
CURRENT APPLICATION NUMBER: PCT/US02/17486  
CURRENT FILING DATE: 2002-06-14  
PRIOR APPLICATION NUMBER: US 60/295,007  
PRIOR FILING DATE: 2001-04-06  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: Patentin version 3.1  
SEQ ID NO: 1  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Fluorogenic substrate  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1) ..(1)  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (4) ..(4)  
OTHER INFORMATION:  
PCT-US02-17486-1

Query Match Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy |||||  
Db ||||| DEV'D 4

RESULT 15  
PCT-US02-17892-1  
Sequence 1, Application PCT/US02/17892  
GENERAL INFORMATION:  
APPLICANT: Cytovia, Inc.  
APPLICANT: Cai, Sui Xiong  
APPLICANT: Zhang, Han Zhong  
APPLICANT: Drew, John A.  
APPLICANT: Reddy, P. Sanjeeva  
APPLICANT: Kasiabhatla, Shailaja  
APPLICANT: Kuemmerle, Jared Daniel  
APPLICANT: Ollis, Kristin P.  
TITLE OF INVENTION: Substituted 3-Aryl-5-aryl-[1,2,4]-oxadiazoles and  
TITLE OF INVENTION: Analogs as Activators of Caspases and Inducers of  
TITLE OF INVENTION: Apoptosis and the Use Thereof  
FILE REFERENCE: 1735.064PC01  
CURRENT APPLICATION NUMBER: PCT/US02/17892  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: US 60/296,479  
PRIOR FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: Patentin version 3.1  
SEQ ID NO: 1  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Fluorogenic substrate  
PCT-US02-17892-1

Query Match Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy |||||  
Db ||||| DEV'D 4

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OM Protein - protein search, using SW model

Run on: May 24, 2004, 14:39:07 ; Search time 13.5 Seconds  
 (without alignments)  
 10.992 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEV'D 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 251736 seqs, 3709738 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
 Listing first 45 summaries

Database :

Pending Patents AA New:  
 1: /cgn2\_6/prodata/1/paa/PCT\_NEW\_COMB.pep:\*

2: /cgn2\_6/prodata/1/paa/US07\_NEW\_COMB.pep:\*

3: /cgn2\_6/prodata/1/paa/US07\_NEW\_COMB.pep:\*

4: /cgn2\_6/prodata/1/paa/US08\_NEW\_COMB.pep:\*

5: /cgn2\_6/prodata/1/paa/US09\_NEW\_COMB.pep:\*

6: /cgn2\_6/prodata/1/paa/US10\_NEW\_COMB.pep:\*

7: /cgn2\_6/prodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	21	100.0	4	1	PCT-US03-20668A-1	Sequence 1, Appl <i>i</i>
2	21	100.0	4	1	PCT-US04-11915-41	Sequence 41, Appl <i>i</i>
3	21	100.0	4	1	PCT-US04-11916-23	Sequence 23, Appl <i>i</i>
4	21	100.0	4	6	US-10-768-976-64	Sequence 64, Appl <i>i</i>
5	21	100.0	4	6	US-10-630-926-14	Sequence 14, Appl <i>i</i>
6	21	100.0	4	6	US-10-626-905-43	Sequence 43, Appl <i>i</i>
7	21	100.0	4	6	US-10-626-258-22	Sequence 22, Appl <i>i</i>
8	21	100.0	4	6	US-10-471-720-1	Sequence 1, Appl <i>i</i>
9	21	100.0	4	6	US-10-030-378-1	Sequence 1, Appl <i>i</i>
10	21	100.0	4	6	US-10-263-330A-43	Sequence 43, Appl <i>i</i>
11	21	100.0	4	6	US-10-146-136-1	Sequence 1, Appl <i>i</i>
12	21	100.0	4	6	US-10-622-9052-43	Sequence 43, Appl <i>i</i>
13	21	100.0	4	6	US-10-816-893-1	Sequence 1, Appl <i>i</i>
14	21	100.0	4	6	US-10-826-909-41	Sequence 41, Appl <i>i</i>
15	21	100.0	4	6	US-10-822-923-23	Sequence 23, Appl <i>i</i>
16	21	100.0	4	6	US-10-829-381-39	Sequence 5, Appl <i>i</i>
17	21	100.0	4	6	US-10-844-470-39	Sequence 39, Appl <i>i</i>
18	21	100.0	4	7	US-60-549-602-4	Sequence 4, Appl <i>i</i>
19	21	100.0	5	1	PCT-US04-0475-15	Sequence 15, Appl <i>i</i>
20	21	100.0	5	6	PCT-US04-04752-19	Sequence 19, Appl <i>i</i>
21	21	100.0	5	6	US-10-684-346-41	Sequence 41, Appl <i>i</i>
22	21	100.0	5	6	US-10-684-346-42	Sequence 42, Appl <i>i</i>
23	21	100.0	5	6	US-10-829-381-76	Sequence 76, Appl <i>i</i>
24	21	100.0	7	1	PCT-US04-11915-42	Sequence 42, Appl <i>i</i>
25	21	100.0	7	1	PCT-US04-11911-44	Sequence 44, Appl <i>i</i>
26	21	100.0	7	1	PCT-US04-11916-24	Sequence 24, Appl <i>i</i>

#### RESULT 1

PCT-US03-20668A-1

Sequence 1, Application PC/TUSS0320668A

GENERAL INFORMATION:

APPLICANT: CYTOVIA, INC.  
 APPLICANT: CAI, SUI XIONG  
 APPLICANT: TSENG, BEN  
 APPLICANT: ZHANG, HAN-ZHONG  
 APPLICANT: KASITHATA, SHAILAJA  
 APPLICANT: OLLIS, KRISTIN P.  
 APPLICANT: SIRISOMA, NILANTHA SUDATH  
 APPLICANT: DREW, JOHN A.

TITLE OF INVENTION: Derivatives of Gambogic Acid And Analogs As Activators of Caspases and Inducers of Apoptosis

FILE REFERENCE: 1735-078PC02

CURRENT APPLICATION NUMBER: PCT/US03-20668A

PRIOR APPLICATION NUMBER: 60/413,649

PRIOR FILING DATE: 2003-07-01

PRIOR FILING DATE: 2002-07-01

PRIOR FILING DATE: 2002-07-01

PRIOR FILING DATE: 2002-09-26

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.1

SEQ ID NO: 1

LENGTH: 4

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: MOD RES

NAME/KEY: MOD RES

LOCATION: (1)-(1)

OTHER INFORMATION: N-terminal acetyl

FEATURE: MOD RES

NAME/KEY: MOD RES

LOCATION: (4)-(4)

OTHER INFORMATION: C-terminal N' -ethoxycarbonyl-Rhodamine 110

PCT-US03-20668A-1

Query Match Similarity 100.0% ; Score 21; DB 1; Length 4;

Best Local Similarity 100.0% ; Pred. No. 2e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEV'D 4

Db 1 DEV'D 4

RESULT 2

PCT-US04-11915-41

Sequence 41, Application PC/TUSS0411915

GENERAL INFORMATION:  
 APPLICANT: Cai, Sui Xiong  
 APPLICANT: Tseng, Ben  
 APPLICANT: Kuemmerle, Jared  
 APPLICANT: Cytovia, Inc.  
 TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis  
 TITLE OF INVENTION: and Screening Assays  
 FILE REFERENCE: 1735.087PC02  
 CURRENT FILING DATE: 2004-04-23  
 PRIOR APPLICATION NUMBER: US 60/484,750  
 PRIOR FILING DATE: 2003-07-07  
 PRIOR APPLICATION NUMBER: US 60/463,649  
 PRIOR FILING DATE: 2003-04-18  
 PRIOR APPLICATION NUMBER: US 60/532,665  
 PRIOR FILING DATE: 2003-12-29  
 PRIOR APPLICATION NUMBER: US 60/463,662  
 PRIOR FILING DATE: 2003-04-18  
 PRIOR APPLICATION NUMBER: US 60/484,749  
 PRIOR FILING DATE: 2003-07-07  
 NUMBER OF SEQ ID NOS: 49  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 41  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Artificial  
 FEATURE:  
 OTHER INFORMATION: Synthetic Peptide  
 PCT-US04-11915-41

Query Match 3  
 Best Local Similarity 100.0%; Score 21; DB 1; Length 4;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEV D 4  
 Db 1 DEV D 4

RESULT 3  
 PCT-US04-11916-23  
 Sequence 23, Application PC/TUS04/11916  
 GENERAL INFORMATION:  
 APPLICANT: Kasibhatla, Shailaja  
 APPLICANT: Cai, Sui Xiong  
 APPLICANT: Tseng, Ben  
 APPLICANT: Jessen, Karayoun Alayi  
 APPLICANT: Maiaratchouk, Serguei  
 APPLICANT: English, Nicole Marion  
 APPLICANT: Kuenmerle, Jared  
 APPLICANT: Kemannitzer, William E.  
 APPLICANT: Zhang, Han-Zhong  
 APPLICANT: Kuenmerle, Jared  
 APPLICANT: Cytovia, Inc.  
 TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis  
 TITLE OF INVENTION: and Screening Assays  
 FILE REFERENCE: 1735.087PC01  
 CURRENT FILING DATE: 2004-04-23  
 PRIOR FILING DATE: 2003-04-18  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 23  
 LENGTH: 4  
 TYPE: PRT

GENERAL INFORMATION:  
 APPLICANT: Artificial  
 OTHER INFORMATION: Synthetic Peptide  
 PCT-US04-11916-23

Query Match 4  
 Best Local Similarity 100.0%; Score 21; DB 1; Length 4;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEV D 4  
 Db 1 DEV D 4

RESULT 4  
 US-10-768-976-64  
 Sequence 64, Application US/10768976  
 GENERAL INFORMATION:  
 APPLICANT: Wood, Keith V.  
 APPLICANT: Los, Georgyi V.  
 APPLICANT: Buleit, Robert F.  
 APPLICANT: Klaubert, Dietter  
 APPLICANT: McDougal, Mark  
 APPLICANT: Zimbrich, Chad  
 APPLICANT: Promega Corporation  
 TITLE OF INVENTION: Covalent Tethering of Functional Groups to Proteins  
 FILE REFERENCE: 341.020US1  
 CURRENT APPLICATION NUMBER: US/10/768,976  
 CURRENT FILING DATE: 2004-01-30  
 PRIOR APPLICATION NUMBER: US 60/444,094  
 PRIOR FILING DATE: 2003-01-31  
 PRIOR APPLICATION NUMBER: US 60/474,659  
 PRIOR FILING DATE: 2003-05-30  
 NUMBER OF SEQ ID NOS: 64  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 64  
 LENGTH: 4  
 TYPE: PRT  
 FEATURE:  
 OTHER INFORMATION: A synthetic peptide  
 US-10-768-976-64

Query Match 4  
 Best Local Similarity 100.0%; Score 21; DB 6; Length 4;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEV D 4  
 Db 1 DEV D 4

RESULT 5  
 US-10-630-926-14  
 Sequence 14, Application US/10630926  
 GENERAL INFORMATION:  
 APPLICANT: RICCARDI, Carlo  
 TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL  
 DEATH PATHWAYS  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSE: BRONDY AND NETMARK, P.L.L.C.  
 STREET: 624 Ninth Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20001  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/630,926  
 FILING DATE: 31-Jul-2003  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/403,861A  
 FILING DATE: 11-Feb-2000  
 APPLICATION NUMBER: PCT/EP98/02490  
 FILING DATE: 27-APR-1998  
 APPLICATION NUMBER: EP 97107033.9  
 FILING DATE: 28-APR-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: YUN, Allen C.  
 REGISTRATION NUMBER: 37,971  
 RECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 FEATURE:  
 OTHER INFORMATION: /note= "the N-terminus is modified by an acetyl group; the C-terminus is modified with a-(4-methyl-coumarin-7- amide)"  
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
 us-10-630-926-14

Query Match 100.0%; Score 21; DB 6; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 6  
 US-10-626-905-43  
 Sequence 43, Application US/10626905  
 GENERAL INFORMATION:  
 APPLICANT: FRANZOZO, GUIDO  
 APPLICANT: DESMABLE, ENRICO  
 APPLICANT: ZAZZERONI, FRANCESCA  
 APPLICANT: PAPA, SALVATORE  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS  
 FILE REFERENCE: 21459-94575  
 CURRENT APPLICATION NUMBER: US/10/626,905  
 CURRENT FILING DATE: 2003-07-25  
 PRIOR APPLICATION NUMBER: PCT/US02/31548  
 PRIOR FILING DATE: 2002-10-02  
 PRIOR APPLICATION NUMBER: 10/263,330  
 PRIOR FILING DATE: 2002-10-02  
 PRIOR APPLICATION NUMBER: 60/328,811  
 PRIOR FILING DATE: 2001-10-12  
 PRIOR APPLICATION NUMBER: 60/326,492  
 PRIOR FILING DATE: 2001-10-02  
 NUMBER OF SEQ ID NOS: 53  
 SOFTWARE: PatentIn Version 3.2  
 SEQ ID NO 43

LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 us-10-626-905-43

Query Match 100.0%; Score 21; DB 6; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 7  
 US-10-626-258-22  
 Sequence 22, Application US/10626258  
 GENERAL INFORMATION:  
 APPLICANT: Snavely, Marshall  
 APPLICANT: Kionsky, Len  
 TITLE OF INVENTION: Enhanced Solubility of Recombinant Proteins  
 FILE REFERENCE: A-725  
 CURRENT APPLICATION NUMBER: US/10/626,258  
 CURRENT FILING DATE: 2003-07-23  
 PRIOR APPLICATION NUMBER: US/09/715,521C  
 PRIOR FILING DATE: 2000-11-17  
 NUMBER OF SEQ ID NOS: 30  
 SEQ ID NO 22  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: caspase 3 protease  
 us-10-626-258-22

Query Match 100.0%; Score 21; DB 6; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 8  
 US-10-471-720-1  
 Sequence 1, Application US/10471720  
 GENERAL INFORMATION:  
 APPLICANT: Cai, Sui Xiong  
 APPLICANT: Reddy, P. Sanjeeva  
 APPLICANT: Drewe, John A.  
 APPLICANT: Nguen, Bao Ngoc  
 APPLICANT: Kasibhatla, Shailla  
 TITLE OF INVENTION: Multifluoro-substituted Chalcones and Analogs as Activators of Caspases and Inducers of Apoptosis and the Use Thereof  
 FILE REFERENCE: 173-054001  
 CURRENT APPLICATION NUMBER: US/10/471,720  
 CURRENT FILING DATE: 2003-09-15  
 PRIOR APPLICATION NUMBER: PCT/US02/07569  
 PRIOR FILING DATE: 2002-03-14  
 PRIOR APPLICATION NUMBER: US 60/275,473  
 PRIOR FILING DATE: 2001-03-14  
 NUMBER OF SEQ ID NOS: 1  
 SOFTWARE: PatentIn Version 3.2  
 SEQ ID NO 1  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Fluorogenic substrate  
 us-10-471-720-1

Query Match 100.0%; Score 21; DB 6; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;

Qy 1 DEVD 4  
 Db 1 DEVD 4

RESULT 9  
 US-10-030-378-1

; Sequence 1; Application US/10030378

; GENERAL INFORMATION:

; APPLICANT: BUE, JEFFREY T.

; TITLE OF INVENTION: DETECTION OF VIRAL STABILITY

; FILE REFERENCE: 20455P

; CURRENT FILING DATE: 2001-11-09

; PRIOR APPLICATION NUMBER: PCT/US00/12638

; PRIOR FILING DATE: 2000-05-10

; PRIOR APPLICATION NUMBER: 6/1134,163

; PRIOR FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: Fast-SEQ for Windows Version 4.0

; SEQ ID NO: 1

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: caspase 3 substrate

US-10-030-378-1

Query Match Score 21; DB 6; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

RESULT 10

US-10-263-330A-43

; Sequence 43; Application US/10263330A

; GENERAL INFORMATION:

; APPLICANT: FRANZOZO, GUIDO

; APPLICANT: DESMAELE, ENRICO

; APPLICANT: ZAZZERONI, FRANCESCA

; APPLICANT: PAPA, SALVATORE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS

; FILE REFERENCE: 21459-94575

; CURRENT APPLICATION NUMBER: US/10/526,905A

; CURRENT FILING DATE: 2003-07-15

; PRIOR APPLICATION NUMBER: PCT/US02/31548

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 10/263,330

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 60/328,811

; PRIOR FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/326,492

; PRIOR FILING DATE: 2001-10-02

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO: 43

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-263-330A-43

Query Match Score 21; DB 6; Length 4;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

RESULT 11

US-10-146-136-1

; Sequence 1; Application US/10146136

; GENERAL INFORMATION:

; APPLICANT: CAI, SUI XIONG

; APPLICANT: ZHANG, HONG

; APPLICANT: KENNITZER, WILLIAM

; GENERAL INFORMATION:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-816-893-1

; Sequence 1; Application US/10816893

; GENERAL INFORMATION:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-626-905A-43

; Sequence 43; Application US/10626905A

; GENERAL INFORMATION:

; APPLICANT: FRANZOZO, GUIDO

; APPLICANT: DESMAELE, ENRICO

; APPLICANT: ZAZZERONI, FRANCESCA

; APPLICANT: PAPA, SALVATORE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS

; FILE REFERENCE: 21459-94575

; CURRENT APPLICATION NUMBER: US/10/526,905A

; CURRENT FILING DATE: 2003-07-15

; PRIOR APPLICATION NUMBER: PCT/US02/31548

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 10/263,330

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 60/328,811

; PRIOR FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/326,492

; PRIOR FILING DATE: 2001-10-02

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO: 43

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-626-905A-43

; Sequence 43; Application US/10626905A

; GENERAL INFORMATION:

; APPLICANT: FRANZOZO, GUIDO

; APPLICANT: DESMAELE, ENRICO

; APPLICANT: ZAZZERONI, FRANCESCA

; APPLICANT: PAPA, SALVATORE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS

; FILE REFERENCE: 21459-94575

; CURRENT APPLICATION NUMBER: US/10/526,905A

; CURRENT FILING DATE: 2003-07-15

; PRIOR APPLICATION NUMBER: PCT/US02/31548

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 10/263,330

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 60/328,811

; PRIOR FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/326,492

; PRIOR FILING DATE: 2001-10-02

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO: 1

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-626-905A-43

; Sequence 43; Application US/10626905A

; GENERAL INFORMATION:

; APPLICANT: FRANZOZO, GUIDO

; APPLICANT: DESMAELE, ENRICO

; APPLICANT: ZAZZERONI, FRANCESCA

; APPLICANT: PAPA, SALVATORE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS

; FILE REFERENCE: 21459-94575

; CURRENT APPLICATION NUMBER: US/10/526,905A

; CURRENT FILING DATE: 2003-07-15

; PRIOR APPLICATION NUMBER: PCT/US02/31548

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 10/263,330

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 60/328,811

; PRIOR FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/326,492

; PRIOR FILING DATE: 2001-10-02

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO: 1

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-626-905A-43

; Sequence 43; Application US/10626905A

; GENERAL INFORMATION:

; APPLICANT: FRANZOZO, GUIDO

; APPLICANT: DESMAELE, ENRICO

; APPLICANT: ZAZZERONI, FRANCESCA

; APPLICANT: PAPA, SALVATORE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS

; FILE REFERENCE: 21459-94575

; CURRENT APPLICATION NUMBER: US/10/526,905A

; CURRENT FILING DATE: 2003-07-15

; PRIOR APPLICATION NUMBER: PCT/US02/31548

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 10/263,330

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 60/328,811

; PRIOR FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/326,492

; PRIOR FILING DATE: 2001-10-02

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO: 1

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-626-905A-43

; Sequence 43; Application US/10626905A

; GENERAL INFORMATION:

; APPLICANT: FRANZOZO, GUIDO

; APPLICANT: DESMAELE, ENRICO

; APPLICANT: ZAZZERONI, FRANCESCA

; APPLICANT: PAPA, SALVATORE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS

; FILE REFERENCE: 21459-94575

; CURRENT APPLICATION NUMBER: US/10/526,905A

; CURRENT FILING DATE: 2003-07-15

; PRIOR APPLICATION NUMBER: PCT/US02/31548

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 10/263,330

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 60/328,811

; PRIOR FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/326,492

; PRIOR FILING DATE: 2001-10-02

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO: 1

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-626-905A-43

; Sequence 43; Application US/10626905A

; GENERAL INFORMATION:

; APPLICANT: FRANZOZO, GUIDO

; APPLICANT: DESMAELE, ENRICO

; APPLICANT: ZAZZERONI, FRANCESCA

; APPLICANT: PAPA, SALVATORE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS

; FILE REFERENCE: 21459-94575

; CURRENT APPLICATION NUMBER: US/10/526,905A

; CURRENT FILING DATE: 2003-07-15

; PRIOR APPLICATION NUMBER: PCT/US02/31548

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 10/263,330

; PRIOR FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: 60/328,811

; PRIOR FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/326,492

; PRIOR FILING DATE: 2001-10-02

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO: 1

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-626-905A-43

; Sequence 43; Application US/10626905A

; GENERAL INFORMATION:

; APPLICANT: FRANZOZO, GUIDO

Query Match 100.0%; Score 21; DB 6; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0;

Qy ||||| 1 DEV'D 4  
 Db ||||| 1 DEV'D 4

RESULT 15  
 US-10-826-923-23  
 / SEQUENCE 23, Application US/10826523  
 / GENERAL INFORMATION:  
 / APPLICANT: Kasibhatla, Shailaja  
 / APPLICANT: Cai, Sui Xiong  
 / APPLICANT: Teeng, Ben  
 / APPLICANT: Jessen, Katayoun Alavi  
 / APPLICANT: Maliartchouk, Serguei  
 / APPLICANT: English, Nicole Marion  
 / APPLICANT: Kuemmerle, Jared  
 / APPLICANT: Kemannier, William E.  
 / APPLICANT: Zhang, Han-Zhong  
 / APPLICANT: Kuemmerle, Jared  
 / TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis  
 / TITLE OF INVENTION: and Screening Assays  
 / FILE REFERENCE: 1735.0870001  
 / CURRENT APPLICATION NUMBER: US/10/826,923  
 / CURRENT FILING DATE: 2004-04-19  
 / PRIOR APPLICATION NUMBER: 60/463,687  
 / PRIOR FILING DATE: 2003-04-18  
 / NUMBER OF SEQ ID NOS: 31  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO 23  
 / LENGTH: 4  
 / TYPE: PRT  
 / ORGANISM: Artificial  
 / FEATURE:  
 / OTHER INFORMATION: Fluorogenic substrate  
 US-10-816-893-1

Query Match 100.0%; Score 21; DB 6; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0;

Qy ||||| 1 DEV'D 4  
 Db ||||| 1 DEV'D 4

RESULT 14  
 US-10-826-909-41  
 / Sequence 41, Application US/10826909  
 / GENERAL INFORMATION:  
 / APPLICANT: Kasibhatla, Shailaja  
 / APPLICANT: Cai, Sui Xiong  
 / APPLICANT: Teeng, Ben  
 / APPLICANT: Jessen, Katayoun Alavi  
 / APPLICANT: English, Nicole Marion  
 / APPLICANT: Maliartchouk, Serguei  
 / APPLICANT: Jiang, Songchun  
 / APPLICANT: Sirisoma, Nilaanthu Sudath  
 / APPLICANT: Zhang, Han-Zhong  
 / APPLICANT: Kuemmerle, Jared  
 / TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis  
 / TITLE OF INVENTION: and Screening Assays  
 / FILE REFERENCE: 1735.0840002  
 / CURRENT APPLICATION NUMBER: US/10/826,909  
 / CURRENT FILING DATE: 2004-04-19  
 / PRIOR APPLICATION NUMBER: US 60/484,750  
 / PRIOR FILING DATE: 2003-07-07  
 / PRIOR APPLICATION NUMBER: US 60/463,649  
 / PRIOR FILING DATE: 2003-04-18  
 / PRIOR APPLICATION NUMBER: US 60/532,665  
 / PRIOR FILING DATE: 2003-12-29  
 / PRIOR APPLICATION NUMBER: US 60/463,662  
 / PRIOR FILING DATE: 2003-04-18  
 / PRIOR APPLICATION NUMBER: US 60/484,749  
 / PRIOR FILING DATE: 2003-07-07  
 / NUMBER OF SEQ ID NOS: 49  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO 41  
 / LENGTH: 4  
 / TYPE: PRT  
 / ORGANISM: Artificial  
 / FEATURE:  
 / OTHER INFORMATION: Synthetic Peptide  
 US-10-826-909-41

Search completed: May 24, 2004, 14:48:20  
 Job time : 13.5 SECS

GenCore version 5.1.6  
(c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: May 24, 2004, 14:36:18 ; Search time 13.5 Seconds  
(without alignments)  
28.501 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78.1\*

1: pir1\*

2: pir2\*

3: pir3\*

4: pir4\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	21	100.0	16	2	PI0137		protein kinase, 80 calcium-binding protein 4
2	21	100.0	18	2	B34473		hydroxymethylgluta
3	21	100.0	44	2	B43714		hypothetical prote
4	21	100.0	45	2	D95155		hypothetical prote
5	21	100.0	49	2	T21745		34.5K linker prote
6	21	100.0	58	2	PO0129		hypothetical prote
7	21	100.0	60	2	C69169		hypothetical prote
8	21	100.0	67	2	T17388		VILI protein - Dic
9	21	100.0	68	2	B71880		4-oxalocrotonate t
10	21	100.0	68	2	D64635		4-oxalocrotonate t
11	21	100.0	69	2	HB1078		4-oxalocrotonate t
12	21	100.0	74	2	B82829		hypothetical prote
13	21	100.0	75	2	F64032		hypothetical prote
14	21	100.0	76	2	D91267		hypothetical prote
15	21	100.0	76	2	A86108		hypothetical prote
16	21	100.0	76	2	S56355		hypothetical .6K
17	21	100.0	82	2	A46337		sim region ORF1 for
18	21	100.0	86	2	E070966		probable phage pro
19	21	100.0	97	2	E64509		hypothetical prote
20	21	100.0	98	1	WWL11		E7 protein - human
21	21	100.0	98	1	WWL6		E7 protein - human
22	21	100.0	98	1	WWL1		E7 protein - pygmy
23	21	100.0	99	2	E5237		protein translo
24	21	100.0	99	2	F78101		conserved hypothet
25	21	100.0	101	1	WWL13		E7 protein - human
26	21	100.0	101	1	WWL51		E7 protein - human
27	21	100.0	101	2	B96645		Glut tRNA amidotran
28	21	100.0	103	2	F97138		hypothetical prote
29	21	100.0	104	2	A83871		hypothetical prote

#### RESULT 3

Query 1 DEVD 4  
Db 2 DEVD 5

Query Match 100.0%; Score 21; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 21; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1  
PL0137  
protein kinase, 80X - pig (fragment)  
C;Species: Sus scrofa domesticus (domestic Pig)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 18-Jun-1993  
C;Accession: PL0137  
C;Dechert, U.; Weber, M.; Weber-Schaeuffelen, M.; Wolny, B.  
J. Neurochem. 53, 1268-1275, 1989  
A;Title: Isolation and partial characterization of an 80,000-dalton protein kinase from rat liver microsomes v  
A;Reference number: PL0137; PMID: 89361455; PMID: 2769266  
A;Accession: PL0137  
A;Molecule type: protein  
A;Residues: 1-16 <DEC>  
C;Comment: This protein has a novel serine/threonine-specific protein kinase activity.

B43714 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) - *Pseudomonas* sp. (fragment)  
 C;Species: *Pseudomonas* sp.  
 C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 26-May-2000  
 C;Accession: B43714  
 R;Anderson, D.H.; Rodwell, V.W.  
 J;Bacteriol, 171, 6468-6472, 1989  
 A;Title: Nucleotide sequence and expression in *Escherichia coli* of the 3-hydroxy-3-methylglutaryl-CoA reductase gene. A43714; MOLD:90078096; PMID:2687236  
 A;Accession: B43714  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-44 <AND>  
 A;Cross-references: GB:M31807; NID:9151370; PIDN:AAA225894.1; PID:9151371  
 C;Superfamily: Methanococcus jannaschii hydroxymethylglutaryl-CoA reductase (NADPH)  
 C;Keywords: coenzyme A; oxidoreductase

Query Match 100.0%; Score 21; DB 2; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 14 DEVD 17

RESULT 4  
 D95155 hypothetical protein SP1339 [imported] - *Streptococcus pneumoniae* (strain TIGR4)  
 C;Species: *Streptococcus pneumoniae*  
 C;Accession: D95155  
 R;Retelain, H.; Neilson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidman, T.; Umam, L.A.; White, C.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle, S.; Hickey, E.K.; Holt, I.E.  
 Science 293, 498-506, 2001.  
 A;Authors: Loftus, B.J.; Yang, F.; Smith, R.O.; Ventres, J.C.; Dougherty, B.A.; Morrison, A.;Reference number: A550000; MUID:21357209; PMID:11463916  
 A;Accession: D95155  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-45 <KUR>  
 A;Cross-references: GB:AE005672; PIDN:AAK75437.1; PID:914972822; GSPDB:GN00164; TIGR:SP4  
 A;Experimental source: strain TIGR4  
 C;Genetic: A;Gene: SPI339

Query Match 100.0%; Score 21; DB 2; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 19 DEVD 22

RESULT 5  
 T21746 hypothetical protein P35C12.1 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Accession: T21746  
 R;Baynes, C.  
 submitted to the EMBL Data Library, October 1996  
 A;Reference number: 219468  
 A;Accession: T21746  
 A;Molecule type: DNA  
 A;Residues: 1-49 <WIL>  
 A;Cross-references: EMBL:Z81075; PIDN:CA03046.1; GSPDB:GN00019; CESP:F35C12.1  
 A;Experimental source: clone F35C12  
 C;Genetics:

A;Gene: CESP:F35C12.1  
 A;Map position: 1  
 A;Introns: 15/2  
 Query Match 100.0%; Score 21; DB 2; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 33 DEVD 36

RESULT 6  
 D90129 34.5K linker protein - *Fischerella* sp. (fragment)  
 C;Species: *Fischerella* sp.  
 C;Accession: D90129  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 11-Jan-2000  
 C;Eberlein, M.; Kuter, W.  
 R;Gene 94, 133-136, 1990  
 A;Title: Genes encoding both subunits of phycoerythrocyanin, a light-harvesting biliprotein  
 A;Reference number: JQ0163; MUID:9103055; PMID:2121619  
 A;Accession: PC0129  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-58 <EBE>  
 A;Cross-references: GB:M34254  
 C;Superfamily: phycocyanin linker protein cpC3

Query Match 100.0%; Score 21; DB 2; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 13 DEVD 16

RESULT 7  
 C69169 hypothetical protein MTH525 - *Methanobacterium thermoautotrophicum* (strain Delta H)  
 C;Species: *Methanobacterium thermoautotrophicum*  
 C;Accession: D90129  
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Ies, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicair, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
 J;Bacteriol, 179, 7135-7155, 1997  
 A;Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: func A;Reference number: A69000; MUID:98037514; PMID:9371463  
 A;Accession: D69169  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-60 <WTH>  
 A;Cross-references: GB:AE000835; GB:AE000666; PIDN:AAB85031.1; PID:92621586  
 A;Experimental source: strain Delta H  
 C;Genetics:  
 A;Gene: MTH525

Query Match 100.0%; Score 21; DB 2; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 22 DEVD 25

RESULT 8  
 T17388 vRL protein - *Dichelobacter nodosus*  
 C;Species: *Dichelobacter nodosus*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C;Accession: TA17388  
 B;Billington, S.J.; Huggins, A.S.; Johansen, P.A.; Crellin, P.K.; Cheung, J.K.; Katz, M.  
 Infect. Immun. 67, 1277-1286, 1999  
 A;Title: Complete nucleotide sequence of the 27-kilobase virulence related locus (vr1) of *Neisseria meningitidis* serogroup B strain MC58  
 A;Reference number: 218734; MUID:10024571  
 A;Accession: TA17388  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-67 <BUT>  
 A;Cross-references: EMBL:U20246; NID:G34933233; PID:93482870; PIDN: AAC33397.1  
 A;Experimental source: strain A198

Query Match 100.0%; Score 21; DB 2; Length 67;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
 Db 45 DEVD 48

RESULT 11  
 H81078  
 4-oxalocrotonate tautomerase (EC 5.3.2.-) NMB1474 [similarity] - *Neisseria meningitidis*  
 C;Species: *Neisseria meningitidis*  
 C;Accession: H81078; H81863  
 C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 02-Feb-2001  
 C;Ricketts, H.; Saunders, N.J.; Jeffries, A.C.; Nelson, K.B.; Eisen, L.;  
 Hickney, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.P.;  
 Qin, H.; Yamane, J.; Gill, J.; Scarlato, V.; Masianni, V.; Pizza, M.  
 Science 287, 1809-1815, 2000  
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;  
 A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
 A;Reference number: A81000; MUID:20175755; PMID:10710307  
 A;Accession: H81078  
 A;Molecule type: DNA  
 A;Residues: 1-69 <TET>  
 A;Cross-references: GB:AE002497; GB:AB002598; NID:97226712; PIDN:AAF41831.1; PID:97226712  
 A;Experimental source: serogroup B, strain MC58  
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mori, T.;  
 Holt, R.; Hulley, S.; Quail, M.A.; Rajandream, M.; Mungall, K.; Leather, S.; Moul, S.;  
 Nature 404, 502-506, 2000  
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
 A;Reference number: A81775; MUID:2022556; PMID:10761919  
 A;Accession: H81863  
 A;Molecule type: DNA  
 A;Residues: 1-69 <PAR>  
 A;Cross-references: GB:AL162756; GB:AL157959; NID:97380091; PIDN:CAB84913.1; PID:97380091  
 A;Experimental source: serogroup A, strain Z2491  
 C;Genetics:  
 A;Gene: Jhp085.8  
 C;Superfamily: 4-oxalocrotonate tautomerase  
 C;Keywords: aromatic hydrocarbon catabolism; intramolecular oxidoreductase; isomerase  
 F;2-68/Product: 4-oxalocrotonate tautomerase  
 F;2/Active site: Pro #status Predicted

Query Match 100.0%; Score 21; DB 2; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
 Db 47 DEVD 50

RESULT 10  
 D64635  
 4-oxalocrotonate tautomerase (EC 5.3.2.-) HPP0924 [similarity] - *Helicobacter pylori* (strain 945c)  
 C;Species: *Helicobacter pylori*  
 C;Accession: D64635  
 C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 17-Mar-2000  
 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;  
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenna, N.;  
 Sod, J.D.; Kelley, J.M.; Cottrell, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.;  
 Nature 388, 539-547, 1997  
 A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.;  
 A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.  
 A;Reference number: A4520; MUID:97394467; PMID:952155  
 A;Accession: D64335  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-68 <TOM>

A;Cross-references: GB:AE000602; GB:AE000511; NID:92314060; PIDN:AAD07977.1; PID:92314060  
 C;Superfamily: 4-oxalocrotonate tautomerase  
 C;Keywords: aromatic hydrocarbon catabolism; intramolecular oxidoreductase; isomerase  
 F;2-68/Product: 4-oxalocrotonate tautomerase #status Predicted <MAT>  
 F;2/Active site: Pro #status Predicted

Query Match 100.0%; Score 21; DB 2; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
 Db 47 DEVD 50

RESULT 11  
 H81078  
 4-oxalocrotonate tautomerase (EC 5.3.2.-) NMB1474 [similarity] - *Neisseria meningitidis*  
 C;Species: *Neisseria meningitidis*  
 C;Accession: H81078; H81863  
 C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 02-Feb-2001  
 C;Ricketts, H.; Saunders, N.J.; Jeffries, A.C.; Nelson, K.B.; Eisen, L.;  
 Hickney, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.P.;  
 Qin, H.; Yamane, J.; Gill, J.; Scarlato, V.; Masianni, V.; Pizza, M.  
 Science 287, 1809-1815, 2000  
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;  
 A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
 A;Reference number: A81000; MUID:20175755; PMID:10710307  
 A;Accession: H81078  
 A;Molecule type: DNA  
 A;Residues: 1-69 <TET>  
 A;Cross-references: GB:AE002497; GB:AB002598; NID:97226712; PIDN:AAF41831.1; PID:97226712  
 A;Experimental source: serogroup B, strain MC58  
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mori, T.;  
 Holt, R.; Hulley, S.; Quail, M.A.; Rajandream, M.; Mungall, K.; Leather, S.; Moul, S.;  
 Nature 404, 502-506, 2000  
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
 A;Reference number: A81775; MUID:2022556; PMID:10761919  
 A;Accession: H81863  
 A;Molecule type: DNA  
 A;Residues: 1-69 <PAR>  
 A;Cross-references: GB:AL162756; GB:AL157959; NID:97380091; PIDN:CAB84913.1; PID:97380091  
 A;Experimental source: serogroup A, strain Z2491  
 C;Genetics:  
 A;Gene: NMB1474; NMA1685  
 C;Superfamily: 4-oxalocrotonate tautomerase  
 C;Keywords: aromatic hydrocarbon catabolism; intramolecular oxidoreductase; isomerase  
 F;2-68/Product: 4-oxalocrotonate tautomerase  
 F;2/Active site: Pro #status Predicted

Query Match 100.0%; Score 21; DB 2; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
 Db 47 DEVD 50

RESULT 12  
 E82829  
 hypothetical protein XF0242 [imported] - *Xylella fastidiosa* (strain 945c)  
 C;Species: *Xylella fastidiosa*  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C;Accession: E82829  
 C;R;Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Seq.  
 Nature 406, 151-157, 2000  
 A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.  
 A;Reference number: A8215; MUID:20385717; PMID:10910347  
 A;Note: for a complete list of authors see reference number A59328 below  
 A;Accession: E82829

A; Status: Preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-74 <SM>  
 A; Experimental source: GB:AE003878; PIDN:BA838531.1; GSPDB:GN00154  
 R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Alvarenga, R.;  
 Briones, M.R.P.; Bueno, M.R.P.; Camargo, L.E.A.; Carrasco, D.M.; Carrer, P.  
 as Neto, E.; Docaia, C.; El-Dorry, H.; Facinani, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000  
 A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn, J.D.; Junqueira, M.L.; Kemper, B.L.; Kriegler, J.B.; Kuranae, B.E.; Laing, D.;  
 Lachado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.; Mench, C.F.M.; Marino, M.V.; Martins, E.;  
 Martins, E.; Nunes, L.R.; Oliveira, M.A.; Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.;  
 Rodrigues, V.; Ross, A.J.; de Rosa Jr., V.E.; de Sá, R.G.; Santelli, R.V.; Sawada, A.;  
 Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.;  
 Tsuahko, M.H.; Vallada, H.; Van Siuys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;  
 A; Reference number: A59328  
 A; Content: annotation  
 C; Genetics:  
 A; Gene: XP02422  
 Query Match 100.0%; Score 21; DB 2; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 64 DEVD 67  
 RESULT 13

F64032  
 hypothetical protein HI1497 - *Haemophilus influenzae* (strain Rd KW20)  
 C; Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 08-Oct-1999  
 C; Accession: F64032  
 R; Fleisschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.;  
 Gooley, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Gocayne, J.; Weidman, J.M.; Weidman, J.;  
 Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.;  
 Science 268, 496-512, 1995  
 A; Authors: Gneam, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.;  
 A; Reference number: A64000; MUID:9535630; PMID:7542800  
 A; Accession: F64032  
 A; Status: nucleic acid sequence not shown; translation not shown  
 A; Molecule type: DNA  
 A; Residues: 1-75 <TRGR>  
 A; Cross-references: GB:U12826; GB:L42023; PIDN: AAC23137.1; PID:91574327; T

Query Match 100.0%; Score 21; DB 2; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 31 DEVD 34

RESULT 14

D91267  
 hypothetical protein EC55108 [imported] - *Escherichia coli* (strain O157:H7, substrain RI  
 C; Species: *Escherichia coli*  
 C; Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
 C; Accession: D91267  
 R; Hayashi, T.; Makino, K.; Ohnishi, K.; Yokoyama, K.; Han, C.G.;  
 Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.;  
 DNA Res. 8, 11-22, 2001  
 A; Reference number: A99629; MUID:21156231; PMID:11258796  
 A; Accession: D91267  
 A; Status: preliminary  
 A; Molecule type: DNA

Result No.	Score	Query	Match	Length	DB	ID	Description
1	21	100.0	20	1	FIBB_SHEEP	P14470;	P14470;
2	21	100.0	21	1	FIBB_ODOHE	AC	AC
3	21	100.0	60	1	YC60_BRAJA	DT 01-JAN-1990	(Rel. 13, Created)
4	21	100.0	63	1	MLP_BOTPU	DT 01-JAN-1990	(Rel. 13, Last sequence update)
5	21	100.0	67	1	Y858_HELPJ	DT 10-OCT-2003	(Rel. 42, Last annotation update)
6	21	100.0	67	1	Y924_HELPY	DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).	
7	21	100.0	75	1	Y997_HAEIN	GN FGB.	
8	21	100.0	76	1	YODI_ECOLI	OS Ovis aries (Sheep), and	
9	21	100.0	77	1	M50_AMBPS	OS Capra hircus (Goat), and	
10	21	100.0	88	1	EP1B_THEAC	OS Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetarrhadoctyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.	
11	21	100.0	95	1	LM2_HUMAN	NCBI_TaxID:9940, 9925;	
12	21	100.0	97	1	VE7 HPV44	RP SEQUENCE.	
13	21	100.0	97	1	VE7 HPV55	RT "Studies on Fibrinopeptides from mammals,"; Blomback B., Blomback M., Grondahl N.J.;	
14	21	100.0	97	1	YG9_METJU	RL Acta Chem. Scand. 19:1789-1791 (1965).	
15	21	100.0	98	1	VE7 HPV1	CC -: FUNCTION: Fibrinogen has a double function: yielding monomers that	
16	21	100.0	98	1	VE7 HPV6A	CC -: POLYMERIZE into fibrin and acting as a cofactor in platelet aggregation.	
17	21	100.0	98	1	VE7 HPV6B	CC -: HEMEOPERTIDE CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.	
18	21	100.0	98	1	VE7 PCP51	CC -: PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.	
19	21	100.0	101	1	GATC_LACLA	CC DR InterPro: IP002181; Fibrinogen C.	
20	21	100.0	101	1	VE7 HPV13	DR PROSITE; PS00314; FIBRIN_AGC_DOMAIN; PARTIAL.	
21	21	100.0	101	1	VE7 HPV51	DR KW Blood coagulation; Plasma; Sulfation.	
22	21	100.0	105	1	DBH_TREPA	FT PEPTIDE 1 20	
23	21	100.0	105	1	GNNI_NETTL	FT MOD_RES 5 5	
24	21	100.0	105	1	VE7 HPV50	FT NON_TER 20 20	
25	21	100.0	105	1	VE7 HPV53	SQ SEQUENCE 20 AA; FCFSB6PFODE6627 CRC64;	
26	21	100.0	105	1	VE7 HPV56	Qy 1 DEVD 4	
27	21	100.0	113	1	CAV_RALSO	Qy 6 DEVD 9	
28	21	100.0	113	1	VE7 HPV51	Db	
29	21	100.0	119	1	PSYC_ECOLI	RESULT 2	
30	21	100.0	129	1	YSX1_CABEL	DBH_ODOHE ID P14476;	
31	21	100.0	133	1	ATPE_MCGE	AC P14476; FIBB_ODOHE STANDARD;	
32	21	100.0	135	1	RSE_HALMA	AC P14476; DT 01-JAN-1990 (Rel. 13, Created)	
33	21	100.0	138	1	YFPO_ECOLI	AC P14476; DT 01-FEB-1994 (Rel. 28, Last sequence update)	
						DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).	
						GN FGB.	
						OS Odocoileus hemionus (Mule deer) (Black-tailed deer).	

## ALIGNMENTS

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : SwissProt\_42.2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result No.

Score

Query

Match

Length

DB

ID

Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	21	100.0	20	1	FIBB_SHEEP	P14470;	P14470;
2	21	100.0	21	1	FIBB_ODOHE	AC	AC
3	21	100.0	60	1	YC60_BRAJA	DT 01-JAN-1990	(Rel. 13, Created)
4	21	100.0	63	1	MLP_BOTPU	DT 01-JAN-1990	(Rel. 13, Last sequence update)
5	21	100.0	67	1	Y858_HELPJ	DT 10-OCT-2003	(Rel. 42, Last annotation update)
6	21	100.0	67	1	Y924_HELPY	DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).	
7	21	100.0	75	1	Y997_HAEIN	GN FGB.	
8	21	100.0	76	1	YODI_ECOLI	OS Ovis aries (Sheep), and	
9	21	100.0	77	1	M50_AMBPS	OS Capra hircus (Goat), and	
10	21	100.0	88	1	EP1B_THEAC	OS Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetarrhadoctyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.	
11	21	100.0	95	1	LM2_HUMAN	NCBI_TaxID:9940, 9925;	
12	21	100.0	97	1	VE7 HPV44	RP SEQUENCE.	
13	21	100.0	97	1	VE7 HPV55	RT "Studies on Fibrinopeptides from mammals,"; Blomback B., Blomback M., Grondahl N.J.;	
14	21	100.0	97	1	YG9_METJU	RL Acta Chem. Scand. 19:1789-1791 (1965).	
15	21	100.0	98	1	VE7 HPV1	CC -: FUNCTION: Fibrinogen has a double function: yielding monomers that	
16	21	100.0	98	1	VE7 HPV6A	CC -: POLYMERIZE into fibrin and acting as a cofactor in platelet aggregation.	
17	21	100.0	98	1	VE7 HPV6B	CC -: HEMEOPERTIDE CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.	
18	21	100.0	98	1	VE7 PCP51	CC -: PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.	
19	21	100.0	101	1	GATC_LACLA	CC DR InterPro: IP002181; Fibrinogen C.	
20	21	100.0	101	1	VE7 HPV13	DR PROSITE; PS00314; FIBRIN_AGC_DOMAIN; PARTIAL.	
21	21	100.0	101	1	VE7 HPV51	DR KW Blood coagulation; Plasma; Sulfation.	
22	21	100.0	105	1	DBH_TREPA	FT PEPTIDE 1 20	
23	21	100.0	105	1	GNNI_NETTL	FT MOD_RES 5 5	
24	21	100.0	105	1	VE7 HPV50	FT NON_TER 20 20	
25	21	100.0	105	1	VE7 HPV53	SQ SEQUENCE 20 AA; FCFSB6PFODE6627 CRC64;	
26	21	100.0	113	1	CAV_RALSO	Qy 1 DEVD 4	
27	21	100.0	113	1	VE7 HPV51	Qy 6 DEVD 9	
28	21	100.0	119	1	PSYC_ECOLI	Db	
29	21	100.0	129	1	YSX1_CABEL	RESULT 2	
30	21	100.0	133	1	ATPE_MCGE	DBH_ODOHE ID P14476;	
31	21	100.0	135	1	RSE_HALMA	AC P14476; FIBB_ODOHE STANDARD;	
32	21	100.0	138	1	YFPO_ECOLI	AC P14476; DT 01-JAN-1990 (Rel. 13, Created)	
33	21	100.0	138	1	Odocoileus hemionus (Mule deer) (Black-tailed deer).	AC P14476; DT 01-FEB-1994 (Rel. 28, Last sequence update)	

DR EMBL; AP005939; BAC45525.1; - .

DR HAMAP; MF\_00649; - ; 1.

DR InterPro; IPR005584; DUF329.

DR Pfam; PF03884; DUF329; 1.

KW Hypothetical protein; Zinc; Metal-binding; Complete proteome.

FT METAL 15 15 ZINC (BY SIMILARITY).

FT METAL 18 18 ZINC (BY SIMILARITY).

FT METAL 30 30 ZINC (BY SIMILARITY).

FT METAL 34 34 ZINC (BY SIMILARITY).

FT SEQUENCE 60 AA; 6692 MW; C7D5FFEE0278B1D9 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 60;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0;

Matches 4; Conservative 0; Sensitive 0;

Qy 1 DEV0 4

Db 54 DEV0 57

RESULT 4

MIP\_BOTAS STANDARD; ERT; 63 AA.

ID MIP\_BOTAS P81077; Created)

AC MIP\_BOTAS P81077; Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DB Myotoxin inhibitor protein MIP

OS Bothrops asper (Terciopelo).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothropidae;

OC NCBITaxID=8722;

OX [1]

RN RP

SEQUENCE.

TISSUE=Blood;

MEDLINE=97439729; PubMed=9307037;

RA Lizano S.; Lemonte B.; Fox J.W.; Gutierrez J.M.;

RT "Biochemical characterization and pharmacological properties of the snake phospholipase A2 myotoxin inhibitor from the plasma of the snake Bothrops asper.",

RT Biochem. J. 326:853-859 (1997).

CC -- FUNCTION: Binds to and neutralizes the activities of basisc phospholipase A2 (PLA2) myotoxin isoforms.

CC -- SUBUNIT: Oligomer composed of five 23-25 kDa subunits.

CC -- SUBCELLULAR LOCATION: Secreted.

CC -- SIMILARITY: Contains 1 C-type lectin family domain.

CC GLYCOPROTEIN; Plasma; Lectin.

RW SEQUENCE 63 AA; 7154 MW; E1E6A75D8489CB6 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 63;

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0;

Matches 4; Conservative 0; Sensitive 0;

Qy 1 DEV0 4

Db 54 DEV0 4

RESULT 5

Y858\_HELP1 STANDARD; ERT; 67 AA.

ID Y858\_HELP1 Q9ZKS7; Created)

AC Q9ZKS7; Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Probable taxonomer JHP0858 (EC 5.3.2.-).

GN JHP0858

OS Helicobacter pylori J99 (Campylobacter pylori J99).

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacter.

OC Helicobacteraceae; Helicobacter.

OC NCBITaxID=85963;

RN [1]

SEQUENCE FROM N.A. PubMed=9923682;  
 RX MEDLINE=9120557; King B.L., Brown B.D., Doig P.C.,  
 RA Alm R.A., Ling L.-S.L., Moir D.T., Guild B.C., deJonge B.L., Carmel G.,  
 RA Smith D.R., Neenan B., Guild B.C., Uria-Nickel M., Mills D.M., Ives C.,  
 RA Tummino R.J., Caruso A., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
 RA Trust T.J.,  
 RT "Genomic sequence comparison of two unrelated isolates of the human  
 RT gastric pathogen *Helicobacter pylori*.";  
 RL 39:176-180(1999).

CC

-1- SIMILARITY: Belongs to the tautomerase family.

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 or send an email to license@isb-sib.ch).

CC

EMBL: AE001515; AA006434.1; -.

DR HAMAP; MF:00718; -; 1.

DR InterPro; IPR004370; Taut.

DR Pfam; PF03361; Tautomerase; 1.

DR ProDom; PD0404143; Taut; 1.

DR TIGRFAMS; TIGR00013; taut; 1.

KW Isomerase; Complete proteome.

FT INIT MET 0 BY SIMILARITY.

FT ACT SITE 1 BY SIMILARITY.

SQ SEQUENCE 67 AA; 7394 MW; CATALYTIC BASE (BY SIMILARITY).

Query Match 100.0%;

Best Local Similarity 100.0%;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Query 1 DEVD 4

Db 46 DEVD 49

RESULT 6

Y924\_HELPPY STANDARD

PRT; 67 AA.

ID Y924\_HELPPY

SEQUENCE FROM N.A.

STRAIN=RD / ATCC 700392;

MEDLINE=97394467;

PubMed=12522185;

RA AC 025581;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Probable tautomerase HP024 (EC 5.3.2.-).

GN 09294.

OS *Helicobacter pylori* (Campylobacter pylori).OC Bacteria; Proteobacteria; *Escherichia*; *Campylobacteriales*;OC *Helicobacteraceae*; *Helicobacter*.

OX NCBI\_TaxID=210;

RN 11

RP SEQUENCE FROM N.A.

RC STRAIN=RD / KW20 / ATCC 51907;

RX MEDLINE=95350630; PubMed=7542800;

RA Fleischmann R.D., Adams C.J., Tomb J.-P., Dougherty B.A., Merrick J.M.,

RA Kerlavage A.R., Bult C.J., Tomb J.-P., Dougherty B.A., Merrick J.M.,

RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

RA Weidman J.D., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,

RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

RA Fine L.D., Fritchman J.L., Fritchman J.L., Geochagen N.S.M.,

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

RA Venter J.C.;

RT "Whole-genome random sequencing and assembly of *Haemophilus influenzae*

RT Rd.";

RL Science 269:496-512(1995).

CC -1- SIMILARITY: Contains 1 dksA/truA-type zinc finger.

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or send an email to license@isb-sib.ch).

CC EMBL: U33826; AAC3137.1; -.

DR PIR; F64032; F64032.

DR TIGR; H11497; -.

DR InterPro; IPR000962; Znf\_Dsfa\_trAr.

DR Pfam; PF01258; zf\_dksA\_trAr.1.

SEQUENCE FROM N.A. PubMed=9923682;  
 RX MEDLINE=9120557; King B.L., Brown B.D., Doig P.C.,  
 RA Alm R.A., Neenan B., Guild B.C., deJonge B.L., Carmel G.,  
 RA Smith D.R., Quackenbush J., Kerkhoff K.A., Klenk H.-P., Sutton G.G.,  
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
 RA Trust T.J.,  
 RT "Genomic sequence comparison of two unrelated isolates of the human  
 RT gastric pathogen *Helicobacter pylori*.";

CC

-1- SIMILARITY: Belongs to the tautomerase family.

CC

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CC EMBL: AE000002; ADD07977.1; -.

DR PIR; D64635; D64635.

DR HAMAP; MF:00718; -; 1.

DR InterPro; IPR004370; Taut.

DR Pfam; PF01351; Tautomerase; 1.

DR Problem; PD404143; Taut; 1.

DR TIGRFAMS; TIGR00013; taut; 1.

KW Isomerase; Complete proteome.

FT INIT MET 0 BY SIMILARITY.

FT ACT SITE 1 BY SIMILARITY.

SQ SEQUENCE 67 AA; 7380 MW; CATALYTIC BASE (BY SIMILARITY).

Query Match 100.0%;

Best Local Similarity 100.0%;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Query 1 DEVD 4

Db 46 DEVD 49

RESULT 6

Y924\_HELPPY STANDARD

PRT; 67 AA.

ID Y924\_HELPPY

SEQUENCE FROM N.A.

STRAIN=RD / ATCC 700392;

MEDLINE=97394467;

PubMed=12522185;

RA AC 025581;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Probable tautomerase HP024 (EC 5.3.2.-).

GN 09294.

OS *Helicobacter pylori* (Campylobacter pylori).OC Bacteria; Proteobacteria; *Escherichia*; *Campylobacteriales*;OC *Helicobacteraceae*; *Helicobacter*.

OX NCBI\_TaxID=210;

RN 11

RP SEQUENCE FROM N.A.

RC STRAIN=RD / KW20 / ATCC 51907;

RX MEDLINE=95350630; PubMed=7542800;

RA Fleischmann R.D., Adams C.J., Tomb J.-P., Dougherty B.A., Merrick J.M.,

RA Kerlavage A.R., Bult C.J., Tomb J.-P., Dougherty B.A., Merrick J.M.,

RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

RA Weidman J.D., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,

RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

RA Fine L.D., Fritchman J.L., Fritchman J.L., Geochagen N.S.M.,

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

RA Venter J.C.;

RT "The complete genome sequence of the gastric pathogen *Helicobacter*RT pylori.";

RT "The complete genome sequence of the tautomerase family.

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or send an email to license@isb-sib.ch).

CC EMBL: U33826; AAC3137.1; -.

DR PIR; F64032; F64032.

DR TIGR; H11497; -.

DR InterPro; IPR000962; Znf\_Dsfa\_trAr.

DR Pfam; PF01258; zf\_dksA\_trAr.1.

PRINTS; PRO00618; DK5ANZINGER; 1.  
 DR PROSITE; P0110; DK5A-TRARZN FINGER; 1.  
 DR Hypothetical protein; Zinc-Finger; Complete proteome.  
 DR ZN FINGER 43 67 TRAR/DKSA-TYPE.  
 SEQUENCE 75 AA; 8405 MW; 9F6DAD6F2C02C626 CRC64;  
 DR ECO 100.0%; Score 21; DB 1; Length 75;  
 DR Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 DR Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DR Qy 1 DEVD 4  
 DR 31 DEVD 34  
 DR

RESULT 8  
 YIDI\_ECOLI STANDARD; PRT; 76 AA.  
 AC P30273;  
 DT 01-FEB-1995 (Rel. 31. Created)  
 DT 01-FEB-1995 (Rel. 31. Last sequence update)  
 DT 16-OCT-2001 (Rel. 40. Last annotation update)  
 DR Hypothetical protein YIDI.  
 GN YIDI OR B4126 OR Z5738 OR ECSS5108.  
 OS Escherichia coli, and  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Bacteroidales; Escherichia.  
 OC Enterobacteriaceae; Escherichia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX M2DLINN=95-34362; PubMed=7610040;  
 RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,  
 RA Blattner F.R.,  
 RT "Analysis of the Escherichia coli genome VI: DNA sequence of the  
 RT region from 92.8 through 100.1995.";  
 RL Nucleic Acids Res. 23:2105-2119(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=211074935; PubMed=11205551;  
 RA Perna N.T., Plunkett G., Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Grotbeck E.T., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalta E.T., Potamitis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.,  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";  
 RL Nature 409:519-533 (2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / RIMD 0509952;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H., Ogasawara N., Yasunaga T.,  
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli  
 O157:H7 and genomic comparison with a laboratory strain K-12.";  
 RL DNA Res. 8:1-22(2001).  
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 CC U140370; AAA7026.1; -.  
 DR EMBL; AE00045; AAC707087.1; -.  
 DR EMBL; AE005646; AAG59325.1; -.

RESULT 9  
 MP5A\_AMBPS STANDARD; PRT; 77 AA.  
 AC P43174;  
 DT 01-NOV-1995 (Rel. 32. Created)  
 DT 01-NOV-1995 (Rel. 42. Last sequence update)  
 DT 10-OCT-2003 (Rel. 42. Last annotation update)  
 DR Pollen allergen Amb P 5a precursor (Amb P Va).  
 OS Ambrosia psilostachya (Western ragweed).  
 OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Streptophyta; Ambrosia.  
 OC Ambrosia psilostachya (Western Ragweed) pollen.;"  
 RT Ambrosia psilostachya (Western Ragweed) pollen.;"  
 RL J. Immunol. 152:288-289 (1994).  
 CC -!- ALLERGEN: Causes an allergic reaction in human.  
 CC SEQUENCE FROM N.A., AND SUBSEQUENCE OF 23-63.  
 RC TISSUE=Polleni.  
 RX MEDLINE=34194048; PubMed=7511632;  
 RA Ghosh B., Rafnar T., Perry M.P., Bassolino-Klimas D.,  
 RA Metzler W.J., Klapser D.G., March D.G.;  
 RT "Immunologic and molecular characterization of Amb P V allergens from  
 RT Ambrosia psilostachya (Western Ragweed) pollen.";  
 RL J. Immunol. 152:288-289 (1994).  
 CC -!- ALLERGEN: Causes an allergic reaction in human.  
 CC SEQUENCE FROM N.A.  
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 CC L24465; AAA20065.1; -.  
 DR EMBL; L24466; AAA20067.1; -.  
 DR HSSP; P1014; IBBG; Amb V allergen.  
 DR Interpro; IPR00561; Amb V allergen.  
 DR Pfam; PF03913; Amb V allergen; 1.  
 DR ProDom; PD01850; Amb V allergen; 1.  
 DR Allergen; Signal.  
 FT SIGNAL 1 22 POLLEN ALLERGEN AMB P 5A.  
 FT CHAIN 23 77  
 FT DISULFID 26 61 BY SIMILARITY.  
 FT DISULFID 33 48 BY SIMILARITY.  
 FT DISULFID 40 54 BY SIMILARITY.  
 FT DISULFID 41 65 BY SIMILARITY.  
 FT VARIANT 59 59 E -> K (IN CLONE A3)  
 SQ SEQUENCE 77 AA; 8710 MW; 2D8376EB65D9A00F CRC64;  
 DR Qy 1 DEVD 4  
 DR 16 DEVD 19  
 DR

RESULT 10	BF1B THEAC	STANDARD;	PRT;	88 AA.
AC Q9HKN1;				
ID BF1B THEAC				
DT 16-OCT-2001 (Rel. 40, Created)				
DT 16-OCT-2001 (Rel. 40, Last sequence update)				
DT 28-FEB-2003 (Rel. 41, Last annotation update)				
DE Elongation factor 1-beta (EF-1-beta).				
GN EF1B OR T0566.				
OS Thermoplasma acidophilum.				
OC Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;				
OC Thermoplasmataceae; Thermoplasma.				
OX NCBI_TaxID=2303;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=DSM 1728;				
RX MEDLINE=20479972; PubMed=11029001;				
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,				
RA Newes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.,				
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum."				
RT Nature 407:508-513 (2000).				
CC FUNCTION: Promotes the exchange of GDP for GTP in EF-1-alpha/GDP, thus allowing the regeneration of EF-1-alpha/GTP that could then be used to form the ternary complex EF-1-alpha/GTP/ACtRNA (By similarity).				
CC - SIMILARITY: Belongs to the EF-1-beta/EF-1-delta family.				
CC -----				
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CC -----				
DR EMBL: AL44064; CAC1706.1; ALT_INIT.				
DR HSSP: Q27734; IGH8.				
DR HAMAP: MF_00043; -;				
DR InterPro: IPR004542; aEF-1-beta.				
DR InterPro: IPR001326; EF1_BD.				
DR PF00736; BF1B; 1.				
DR TIGRFAMs: TIGRFAM0489; aEF-1_beta; 1.				
DR Elongation factor; protein biosynthesis; Complete proteome.				
SEQUENCE 88 AA; 9749 MW; 572357C1BAD5DA7CR64;				
SQ -----				
Query Match Similarity 100.0%; Score 21; DB 1; Length 88;				
Best Local Similarity 100.0%; Pred 0.1.9e+02;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY 1 DEVD 4				
Db 40 DEVD 43				
RESULT 11				
LSM2_HUMAN STANDARD;			PRT;	95 AA.
ID LSM2_HUMAN				
AC Q9Y333;				
DT 16-OCT-2001 (Rel. 40, Created)				
DT 16-OCT-2001 (Rel. 40, Last sequence update)				
DT 10-OCT-2003 (Rel. 42, Last annotation update)				
DE U6 snRNA-associated Sm-like protein LSM2 (Small nuclear ribonucleic protein D homolog) (G7b) (SnRNP core SM-Xs).				
DE LSM2 OR C00R28 OR G7b.				
GN Homo sapiens (Human).				
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OC NCBI_TaxID=9606;				
OX NCBI_TaxID=9606;				
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				

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RE

MEDLINE=96337999; PubMed=8668087;

RA Bult C.J., White O., Olsen G.J., Clayton R.A., Fleischmann R.D., Sutton G.J., Blake J.A., FitzGerald L.M., Clayton J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-P., Adams M.D., Reich C.I., Overbeek R., Kirkpatrick N.S.M., Weidman J.G., Merrick J.M., Glodck A., Scott J.L., Goedhagen N.S.M., Weidman J.P., Subramanian J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts C.M., Hurst M.A., Kaine P.W., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii." RT

Science 273:1058-1073 (1996).

RL

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CC

DR EMBL: U67607; AAB99704; 1; -.

DR PIR: E645059; E645059.

DR TIGR: MJ1679; -.

KW Hypothetical protein; Complete Proteome.

SQ SEQUENCE 97 AA; 11880 MW; 64C59303B9101F00 CRC64;

Query Match 100.0% ; Score 21; DB 1; Length 97;

Best Local Similarity 100.0% ; Prod. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 82 DEVD 85

RESULT 15

VB7 HPV11 STANDARD; PRT; 98 AA..

ID VB7 HPV11

AC P04020;

DT 23-OCT-1986 (Rel. 02, Created)

DT 23-OCT-1986 (Rel. 02, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE B7 protein.

GN E7.

OS Human Papillomavirus type 11.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI\_TAXID:10580;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE:861181601; PubMed=3008427;

RA Dartmann K.; Schwarz E.; Gissmann L.; Zur Hausen H.;

RT "The nucleotide sequence and genome organization of human papilloma virus type 11." RT

RT Virology 151:12-130(1986).

RN [2]

RP SEQUENCE FROM N.A.

RA File K.H.; Fan L.; Fritsch M.H.; Bryan J.; Brown D.R.;

RL Submitted (CCT-1994) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING ACTIVITIES.

CC -!- SIMILARITY: LOCAL WITH ADENOVIRUS E1A AND SV40 LT.

CC

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CC

DR EMBL: M14119; AAA46938; 1; -.

```

DR  EMBL; L26108; AAA21704.1; -
DR  PIR; A03690; W7NLL1;
DR  InterPro; IPR0000148; Papvi_E7
DR  PFAM; PF05227; E7;
DR  Early protein; Trans-acting fac
KW  DNA-binding; Trans-acting fac
KW
FT  SITE      58      61
FT  SITE      91      94
SQ  SEQUENCE  98 AA; 10889 MW;
SQ

Query Match          100.0%/
Best Local Similarity 100.0%/
Matches 4; Conservative 0
Qy   1  DEVD 4
Db   35  DEVD 38

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Search completed: May 24, 2004, 14:45  
Job time : 11.5 secs



RESULT 2		RESULT 3		RESULT 4		RESULT 5	
Q51913	Q51913; PRELIMINARY; PRT; 44 AA.	Q49798	Q49798; PRELIMINARY; PRT; 45 AA.	Q97Q87	Q97Q87; PRELIMINARY; PRT; 45 AA.	QBFV6	QBFV6; PRELIMINARY; PRT; 45 AA.
AC	Q51913; ID: 01-NOV-1996 (TREMBLrel. 01, Created)	AC	Q49798; ID: 01-JUN-1998 (TREMBLrel. 06, Created)	AC	Q97Q87; ID: 01-MAR-2003 (TREMBLrel. 23, Created)	AC	QBFV6; ID: 01-MAR-2003 (TREMBLrel. 23, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)	DT	01-OCT-2001 (TREMBLrel. 18, Last sequence update)	DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT	01-OCT-2001 (TREMBLrel. 18, Last annotation update)	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	HMG-CoA reductase (Fragment).	DE	HMG-CoA reductase (Fragment).	DE	Hypothetical protein SP1339.	DE	Hypothetical protein SP1339.
OS	Pseudomonas mevalonii	OS	Pseudomonas mevalonii	OS	Streptococcus pneumoniae	OS	Streptococcus pneumoniae
OX	Bacteria; Proteobacteria.	OX	Bacteria; Proteobacteria.	OX	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus	OX	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus
NCBI TaxID=2044;				NCBI TaxID=1313;			NCBI TaxID=1313;
RN	[1]			[1]			[1]
SEQUENCE FROM N.A.		SEQUENCE FROM N.A.		SEQUENCE FROM N.A.		SEQUENCE FROM N.A.	
RX	SEQUENCE FROM N.A. PubMed=26872316;	RX	SEQUENCE FROM N.A. PubMed=26872316;	RX	SEQUENCE FROM N.A. PubMed=21335709; PMID=11463916;	RX	SEQUENCE FROM N.A. PubMed=21335709; PMID=11463916;
RA	Anderson D.H.; Rodwell V.W.;	RA	Anderson D.H.; Rodwell V.W.;	RA	Tettelin H.; Nelson K.E.; Paulsen I.T.; Eisen J.A.; Read T.D.; Peterson S.; Heidelberg J.; Deboy R.T.; Dodson R.J.; Durkin A.S.; Gwinn M.; Kolonay J.F.; Nelson W.C.; Peterson J.D.; Umayam L.A.; White O.; Salzberg S.L.; Lewis M.R.; Radune D.; Holtapple B.; Khorri H.; Wolf A.M.; Utterback T.R.; Hansen C.L.; McDonald L.A.; Feldblyum T.V.; Angiuoli S.; Dickinson T.; Holt I.E.; Loftus B.J.; Yang F.; Smith H.O.; Venter J.C.; Dougherty B.A.; Morrison D.A.; Hollingshead S.K.; Fraser C.M.; RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";	RA	Tettelin H.; Nelson K.E.; Paulsen I.T.; Eisen J.A.; Read T.D.; Peterson S.; Heidelberg J.; Deboy R.T.; Dodson R.J.; Durkin A.S.; Gwinn M.; Kolonay J.F.; Nelson W.C.; Peterson J.D.; Umayam L.A.; White O.; Salzberg S.L.; Lewis M.R.; Radune D.; Holtapple B.; Khorri H.; Wolf A.M.; Utterback T.R.; Hansen C.L.; McDonald L.A.; Feldblyum T.V.; Angiuoli S.; Dickinson T.; Holt I.E.; Loftus B.J.; Yang F.; Smith H.O.; Venter J.C.; RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";
RA	"Nucleotide sequence and expression in <i>Escherichia coli</i> of the 3'-hydroxy-3-methylglutaryl coenzyme A lyase gene of <i>Pseudomonas mevalonii</i> ." J. Bacteriol. 171: 6458-6472 (1989).	RA	"Nucleotide sequence and expression in <i>Escherichia coli</i> of the 3'-hydroxy-3-methylglutaryl coenzyme A lyase gene of <i>Pseudomonas mevalonii</i> ." J. Bacteriol. 171: 6458-6472 (1989).	RA	RT "Nucleotide sequence and expression in <i>Escherichia coli</i> of the 3'-hydroxy-3-methylglutaryl coenzyme A lyase gene of <i>Pseudomonas mevalonii</i> ." J. Bacteriol. 171: 6458-6472 (1989).	RA	RT "Nucleotide sequence and expression in <i>Escherichia coli</i> of the 3'-hydroxy-3-methylglutaryl coenzyme A lyase gene of <i>Pseudomonas mevalonii</i> ." J. Bacteriol. 171: 6458-6472 (1989).
RT		RT		RT		RT	
RL		RL		RL		RL	
DR	EMBL; M31807; AA25893.1;	DR	EMBL; M31807; AA25893.1;	DR	EMBL; M31807; AA25893.1;	DR	EMBL; M31807; AA25893.1;
GO	GO:0004120; P:hydroxymethylglutaryl-CoA reductase (NADPH) . . . IEA.	GO	GO:0004120; P:hydroxymethylglutaryl-CoA reductase (NADPH) . . . IEA.	GO	GO:0004120; P:hydroxymethylglutaryl-CoA reductase (NADPH) . . . IEA.	GO	GO:0004120; P:hydroxymethylglutaryl-CoA reductase (NADPH) . . . IEA.
DR	GO:0009058; P:biosynthesis IEA.	DR	GO:0009058; P:biosynthesis IEA.	DR	GO:0009058; P:biosynthesis IEA.	DR	GO:0009058; P:biosynthesis IEA.
DR	InterPro; IPR022020; HMG-CoA_red.	DR	InterPro; IPR022020; HMG-CoA_red.	DR	InterPro; IPR022020; HMG-CoA_red.	DR	InterPro; IPR022020; HMG-CoA_red.
DR	InterPro; IPR009229; HMG-CoA_sub_bind.	DR	InterPro; IPR009229; HMG-CoA_sub_bind.	DR	InterPro; IPR009229; HMG-CoA_sub_bind.	DR	InterPro; IPR009229; HMG-CoA_sub_bind.
DR	PFam; PF003365; HMG-CoA_red_1.	DR	PFam; PF003365; HMG-CoA_red_1.	DR	PFam; PF003365; HMG-CoA_red_1.	DR	PFam; PF003365; HMG-CoA_red_1.
FT	NON-TER 1	FT	NON-TER 1	FT	NON-TER 1	FT	NON-TER 1
SEQUENCE	44 AA; 4925 MW; 9722EE2A58DBE9193 CRC64;	SEQUENCE	44 AA; 4925 MW; 9722EE2A58DBE9193 CRC64;	SEQUENCE	45 AA; 5089 MW; F0A7B635C2683F20 CRC64;	SEQUENCE	45 AA; 5089 MW; F0A7B635C2683F20 CRC64;
Query Match	100.0%; Score 21; DB 2; Length 44;	Query Match	100.0%; Score 21; DB 2; Length 44;	Query Match	100.0%; Score 21; DB 16; Length 45;	Query Match	100.0%; Score 21; DB 16; Length 45;
Best Local Similarity	100.0%; Fred. No. 7e+02;	Best Local Similarity	100.0%; Fred. No. 7e+02;	Best Local Similarity	100.0%; Fred. No. 7.2e+02;	Best Local Similarity	100.0%; Fred. No. 7.2e+02;
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 DEVD 4	Qy	1 DEVD 4	Qy	1 DEVD 4	Qy	1 DEVD 4
Db	14 DEVD 17	Db	14 DEVD 17	Db	19 DEVD 22	Db	19 DEVD 22
RESULT 2	Q51913	RESULT 3	Q49798	RESULT 4	Q97Q87	RESULT 5	QBFV6
ID	Q51913; PRELIMINARY; PRT; 44 AA.	ID	Q49798; PRELIMINARY; PRT; 45 AA.	ID	Q97Q87; PRELIMINARY; PRT; 45 AA.	ID	QBFV6; PRELIMINARY; PRT; 45 AA.
AC	Q51913; ID: 01-NOV-1996 (TREMBLrel. 01, Created)	AC	Q49798; ID: 01-JUN-1998 (TREMBLrel. 06, Created)	AC	Q97Q87; ID: 01-OCT-2001 (TREMBLrel. 18, Last sequence update)	AC	QBFV6; ID: 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)	DT	01-OCT-2001 (TREMBLrel. 18, Last sequence update)	DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	HMGR reductase (Fragment).	DE	HMGR reductase (Fragment).	DE	Hypothetical protein SP1339.	DE	Hypothetical protein SP1339.
OS	Bacteria; Proteobacteria.	OS	Bacteria; Proteobacteria.	OS	Brucellales; Brucellaceae; Brucellales.	OS	Brucellales; Brucellaceae; Brucellales.
NCBI TaxID=2044;		NCBI TaxID=2044;		NCBI TaxID=1313;		NCBI TaxID=1313;	
RN	[1]			[1]			[1]
RP		SEQUENCE FROM N.A.		SEQUENCE FROM N.A.		SEQUENCE FROM N.A.	
RA	Romero I.; Fuertes A.; Benito M.J.; Malpica J.; Leyva A.; Paz-Ares J.;	RA	Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicots; rosids; OC	RA	Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicots; rosids; OC	RA	Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicots; rosids; OC
RL	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.	RL	OC	RA	OC	RA	OC
DR	EMBL; Z95798; CAB09230.1; -	DR	OC	RA	OC	RA	OC
DR	GO; GO:0005634; C:nucleus; Brassicaceae; Arabidopsis.	DR	GO; GO:0005634; C:nucleus; Brassicaceae; Arabidopsis.	DR	GO; GO:0005634; C:nucleus; Brassicaceae; Arabidopsis.	DR	GO; GO:0005634; C:nucleus; Brassicaceae; Arabidopsis.
DR	InterPro; IPR001005; Myb-DNA binding.	DR	InterPro; IPR001005; Myb-DNA binding.	DR	InterPro; IPR001005; Myb-DNA binding.	DR	InterPro; IPR001005; Myb-DNA binding.
DR	PFam; PF00249; myb-DNA-binding_1.	DR	PFam; PF00249; myb-DNA-binding_1.	DR	PFam; PF00249; myb-DNA-binding_1.	DR	PFam; PF00249; myb-DNA-binding_1.
DR	PROSITE; PS50090; MYB_3; 1.	DR	PROSITE; PS50090; MYB_3; 1.	DR	PROSITE; PS50090; MYB_3; 1.	DR	PROSITE; PS50090; MYB_3; 1.
FT	NON-TER	FT	NON-TER	FT	NON-TER	FT	NON-TER
SQ	SEQUENCE 45 AA; 5308 MW; A5ABE1509F3D376 CRC64;	SQ	SEQUENCE 45 AA; 5308 MW; A5ABE1509F3D376 CRC64;	SQ	SEQUENCE 45 AA; 5308 MW; A5ABE1509F3D376 CRC64;	SQ	SEQUENCE 45 AA; 5308 MW; A5ABE1509F3D376 CRC64;
Query Match	100.0%; Score 21; DB 10; Length 45;	Query Match	100.0%; Score 21; DB 10; Length 45;	Query Match	100.0%; Score 21; DB 10; Length 45;	Query Match	100.0%; Score 21; DB 10; Length 45;
Best Local Similarity	100.0%; Fred. No. 7.2e+02;	Best Local Similarity	100.0%; Fred. No. 7.2e+02;	Best Local Similarity	100.0%; Fred. No. 7.2e+02;	Best Local Similarity	100.0%; Fred. No. 7.2e+02;
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 DEVD 4	Qy	1 DEVD 4	Qy	1 DEVD 4	Qy	1 DEVD 4

DR TIGR; BRA0821; .  
 KW Hypothetical protein; Complete proteome  
 SEQUENCE 45 AA; 5041 MW; 7FB6874E77F886 CRC64;  
 Query Match 100.0%; Score 21; DB 16; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DEVD 4  
 1 |||  
 Db 3 DEVD 6

RESULT 6  
 ID Q96P95 PRELIMINARY; PRT; 49 AA.  
 AC Q96P95; PRELIMINARY;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Poly (ADP-ribose) Polymerase (Fragment).  
 OS Homo sapiens (Human).  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN SEQUENCE FROM N.A.  
 RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.; Kim Y.H.; Rattus.  
 RT "Characterization of TPA-responsive genes in U937 cells using ordered differential display PCR.";  
 RT SEQUENCES FROM N.A. to the EMBL/GenBank/DBJ databases.  
 RL Submitted: AF401218; AA02174.1; -  
 DR GO:000533; C:nucleus; IEA.  
 DR InterPro: IPR001510; Znf PolyADPpol.  
 DR Pfam: PF00665; ZF-PARP; 1.  
 DR PROSITE: PS50064; PARP\_ZN\_FINGER\_2; 1.  
 FT NON\_TER 1 49  
 FT NON\_TER 1 49  
 SQ SEQUENCE 49 AA; 5300 MW; 68F91BA7DAEDF4A5 CRC64;  
 Query Match 100.0%; Score 21; DB 4; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DEVD 4  
 1 |||  
 Db 34 DEVD 37

RESULT 7  
 ID Q9XVP5 PRELIMINARY; PRT; 49 AA.  
 AC Q9XVP5; PRELIMINARY;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE F35C1.1 protein.  
 DN F35C1.1..  
 OS Caenorhabditis elegans.  
 OC Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae.  
 OC Rhabditidae; Pelioderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6339;  
 RN SEQUENCE FROM N.A.  
 RA Baynes C.; Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2] SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.; PubMed=9851916;  
 RX none;  
 RT "Genome sequence of the nematode *C. elegans*: A platform for

investigating biology.";  
 RL Science 282:2012-2018 (1998).  
 DR EMBL; 281075; CAB03046.1;  
 PIR; T21746; T21746.  
 DR WormPep; F35C12.1.; CB09943.  
 SQ SEQUENCE 49 AA; 5597 MW; 778CB60EE83DFFEBE CRC64;  
 Query Match 100.0%; Score 21; DB 5; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DEVD 4  
 Db 33 DEVD 36

RESULT 8  
 ID Q63952 PRELIMINARY; PRT; 50 AA.  
 AC Q63952; PRELIMINARY;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE Endoplasmic (Fragment).  
 GN GRP94.  
 OS Rattus.  
 OC Bukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RP MEDLINE=9414828; PubMed=8314313;  
 RX DE Vouge M.W.; Yamazaki A.; Bennett S.A.; Chen J.H.; Shwed P.S.,  
 RA Couture C.; Birnboim H.C.;  
 RA Immunoselection of GRP94/endoplasmic from a KNRK cell-specific lambda  
 RT Stil library using antibodies directed against a putative heparanase  
 RT amino-terminal peptide.  
 RL Int. J. Cancer 56 226-294 (1994).  
 DR EMBL; S69315; AAB29919.2; -.  
 FT NON\_TER 50 50  
 SQ SEQUENCE 50 AA; 5478 MW; D8866A965A646117 CRC64;  
 Query Match 100.0%; Score 21; DB 11; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DEVD 4  
 Db 23 DEVD 26

RESULT 9  
 ID Q9IAB6 PRELIMINARY; PRT; 53 AA.  
 AC Q9IAB6; PRELIMINARY;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE SMX5 (Fragment).  
 GN SMX5.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RP Suelthahn H.; Murray B.W.; Klein J.;  
 RA "Analysis of Ancient Mhc Class III Synteny by Mapping of Orthologous  
 RT Genes in the Zebrafish.";  
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF210645; AAF0450.1; -.  
 DR ZFIN; ZDB-GENE-000616-10; smx5.

DR GO:GO:0005634; C:nucleus; IEA.  
 DR GO:GO:0005532; C:small nucleolar ribonucleoprotein complex; IEA.  
 DR GO:GO:0003248; F:pre-mRNA splicing factor activity; IEA.  
 DR GO:GO:0008649; snRNP\_splicing; IEA.  
 DR InterPro; IPR006649; snRNP\_Sm.  
 DR InterPro; IPR01163; snRNP\_Sm.  
 DR PF01423; LSM; 1.  
 DR ProDom; PD020287; snRNP; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 53 53  
 SQ SEQUENCE 53 AA; 6078 MW; E70502074A527393 CRC64;  
 Query Match 100.0%; Score 21; DB 13; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 48 DEVD 51  
 RESULT 10  
 Q981MB\_ PRELIMINARY; PRT; 53 AA.  
 ID Q981MB\_  
 AC Q981MB\_  
 DT 01-OCT-2001 (TREMBLrel. 18, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Hypothetical protein msr234.  
 GN MSR234.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1] SEQUENCE FROM N.A.  
 RP STRAIN=21082930; PubMed=11214968;  
 RX MEDLINE=95115663; PubMed=7816023;  
 RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idesawa A., Itohaki A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 RT Mesorhizobium loti".  
 RT DNA Res. 7:331-338 (2000).  
 DR EMBL; AP002999; BA049483.1; -.  
 XW Hypothetical protein; Complete Proteome.  
 SQ SEQUENCE 53 AA; 5289 MW; B7C5B7886C6D8279 CRC64;  
 Query Match 100.0%; Score 21; DB 16; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 10 DEVD 13  
 RESULT 11  
 Q382558\_ PRELIMINARY; PRT; 54 AA.  
 ID Q382558\_  
 AC Q382558\_  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DB Unidentified ORF15.  
 OS Lactococcus phage bIL67.  
 OC dsDNA viruses; no RNA stage; Caudovirales; Siphoviridae;  
 OC c2-like viruses.  
 OX NCBI\_TaxID=36343;  
 RN [1] SEQUENCE FROM N.A.  
 RP

RX MEDLINE=15111629; PubMed=7812447;  
 RA Schouler C., Ehrlich S.D., Choppin M.C.;  
 RT "Sequence and organization of the lactococcal prolate-headed bIL67  
 Phage genome.";  
 RL Microbiology 140:1061-3069 (1994).  
 DR EMBL; L31769; AAA74352.1; -.  
 SQ SEQUENCE 54 AA; 63738 MW; F2D42F31659BF751 CRC64;  
 Query Match 100.0%; Score 21; DB 9; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 10 DEVD 13  
 RESULT 12  
 Q38280\_ PRELIMINARY; PRT; 54 AA.  
 ID Q38280\_  
 AC Q38280\_  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE B17 protein.  
 OS Lactococcus bacteriophage c2.  
 OC dsDNA viruses; no RNA stage; Caudovirales; Siphoviridae;  
 OC c2-like viruses.  
 OX NCBI\_TaxID=31537;  
 RN [1] SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94036433; PubMed=8221377;  
 RA Ward L.J., Beresford T.P., Lubbers M.W., Jarvis B.D., Jarvis A.W.;  
 RA "Sequence analysis of the lysis gene region of the prolate lactococcal  
 bacteriophage c2".  
 RT "Sequence analysis of the lysis gene region of the prolate lactococcal  
 bacteriophage c2".  
 RN [2] SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95115663; PubMed=7816023;  
 RA Lubbers M.W., Ward L.J., Beresford T.P., Jarvis B.D., Jarvis A.W.;  
 RA "Sequencing and analysis of the cos region of the lactococcal  
 bacteriophage c2."  
 RT "Sequencing and analysis of the cos region of the lactococcal  
 bacteriophage c2."  
 RL Mol. Genet. 245:160-166 (1994).  
 RN [3] SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96086619; PubMed=8534101;  
 RA Lubbers M.W., Waterfield N.R., Beresford T.P., Le Page R.W.,  
 RA Jarvis A.W.;  
 RT "Sequencing and analysis of the prolate-headed lactococcal  
 bacteriophage c2 genome and identification of the structural genes.";  
 RT bacteriophage c2 genome and identification of the structural genes.";  
 RL Appl. Environ. Microbiol. 61:4348-4356 (1995).  
 DR EMBL; L48605; AAA9263.1; -.  
 SQ SEQUENCE 54 AA; 6453 MW; EA5811217531F751 CRC64;  
 Query Match 100.0%; Score 21; DB 9; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DEVD 4  
 Db 10 DEVD 13  
 RESULT 13  
 Q8ANR3\_ PRELIMINARY; PRT; 54 AA.  
 ID Q8ANR3\_  
 AC Q8ANR3\_  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE P0034A04.6 Protein.  
 GN P0034A04.6.

OS *Oryza sativa* (japonica cultivar-group). Embryophyta; Tracheophyta;  
 OC Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoidae; Oryzeae; *Oryza*.  
 OX NCBI\_TaxID=33947;  
 RN [1];  
 RP SEQUENCE FROM N.A.

RC *RA*; *Sasaki T.*; *Matsu moto T.*; *Yamamoto K.*; DNA, chromosome 7, PAC  
 RT clone: 20034A04.;  
 RT Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.  
 RL EMBL: AP003333; BRC: BRC552.1;  
 DR SEQUENCE 54 AA; 6002 MW; 1825F648415E8B CRC64;

Query Match Score 100.0%; Score 21; DB 10; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
 Indels 0;

Qy 1 DEVD 4  
 Db 35 DEVD 38

RESULT 14  
 Q977A0 PRELIMINARY; PRT; 54 AA.  
 ID Q977A0  
 AC 0977A0  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Putative alcohol dehydrogenase.  
 GN STS015.

CS *Sulfolobus tokodaii*. Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

OC *Sulfolobus*.  
 OC NCBI\_TaxID=11955;

RN [1];  
 RP SEQUENCE FROM N.A.

RC STRAIN=JCM 10545 /  
 RX MEDLINE=22456156; PubMed=11572479;  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Fukui S.,  
 RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hoboyama A., Nakazawa R., Nakazawa M., Kato Y.,  
 RA Nagai Y., Nishizawa T., Otsuka T., Tanaka T., Kudo H., Yamazaki J., Kusuda N., Oguchi A.,  
 RA Yoshihizawa T., Tanaka T., Kudo H., Yamazaki J., Kusuda N., Yamagishi A.,  
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,  
 RA Oshima T., Rikuchi H.,  
 RT "Complete genome sequence of an aerobic thermoacidophilic  
 RT Crenarchaeon *Sulfolobus tokodaii* strain7.";  
 RL DNA Res. 8:123-140(2001).

DR EMBL: AP000981; BAB4994.1;  
 DR GO: 0004024; F: alcohol dehydrogenase activity, zinc-dependent; IEA.  
 DR GO: 0008270; F: zinc ion binding; IEA.  
 DR InterPro: IPR004085; Adh zn Family.  
 DR Pfam: PF00107; ADH zinc\_N\_1.  
 KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 54 AA; 6138 MW; 132BC067738F740 CRC64;

Query Match Score 100.0%; Score 21; DB 17; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 DEVD 4  
 Db 16 DEVD 19

RESULT 15  
 Q99H60 PRELIMINARY; PRT; 56 AA.  
 ID Q99H60  
 AC Q99H60;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE RNA-dependent RNA polymerase (fragment).  
 OC Human Picobirnavirus.  
 OC Viruses; dRNA viruses; Picobirnavirus.  
 OX NCBI\_TaxID=145856;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=202-FL-97; PubMed=11080479;  
 RX MEDLINE=20334978; Glass R.I., Monroe S.S.;  
 RA Rosen B.I., Fang Z.Y.;  
 RT "Cloning of human picobirnavirus genomic segments and development of an RT-PCR detection assay.";  
 RL Virology 277:316-329(2000).  
 EMBL: AF246935; AAG33579.1;  
 DR GO: GO:003968; F: RNA-directed RNA polymerase activity; IEA.  
 KW RNA-directed RNA polymerase.  
 FT NON-TER 1 1  
 FT NON-TER 56 56  
 SQ SEQUENCE 56 AA; 6708 MW; 781490BF8BB423A9 CRC64;  
 FT NON-TER 1 1  
 FT NON-TER 56 56  
 SQ SEQUENCE 56 AA; 6708 MW; 781490BF8BB423A9 CRC64;  
 Qy 1 DEVD 4  
 Db 31 DEVD 34

Query Match Score 100.0%; Score 21; DB 12; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;